

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:08:41 ; Search time 14 Seconds

(without alignments)
1128.749 Million cell updates/sec

Title: US-09-623-035-2

Perfect score: 381

Sequence: 1 MTVPSPVPALPLGLGLPR.....HTCFITLGLGLVWGLLT 381

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0 112892

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	301	79.0	381	DAF_HUMAN	P08174 homo sapien
2	85	22.3	340	DAF_PONPY	P49457 pongo pygma
3	13	3.4	507	DAF_CAVPO	Q60401 cavia porce
4	10	2.6	390	DAF1_MOUSE	Q61475 mus musculu
5	10	2.6	407	DAF2_MOUSE	Q61476 mus musculu
6	9	2.4	345	APOR_HUMAN	P02149 homo sapien
7	8	2.1	307	TAL_PSEAE	Q91047 pseudomonas
8	8	2.1	322	ASPG_DETRA	Q91893 delnoccocus
9	8	2.1	503	TGRI_HUMAN	P36897 homo sapien
10	8	2.1	522	PME_PRUPE	Q43062 prunus pers
11	8	2.1	555	UL25_HSV62	P52537 human herpe
12	8	2.1	558	C4BP_RAT	Q63514 rattus norv
13	7	1.8	89	RS1S_PSEPU	O87791 pseudomonas
14	7	1.8	119	B2MG_CEBAL	O77826 cebus albid
15	7	1.8	119	B2MG_CHISA	P37652 chiropotes
16	7	1.8	143	YIBN_ECOLI	O37688 escherichia
17	7	1.8	156	RNP_HUMAN	P07998 homo sapien
18	7	1.8	204	CPCE_SYNP7	Q44116 synechococc
19	7	1.8	219	YGBH_SALT	P18951 salmonella
20	7	1.8	230	CLD2_CANFA	Q95K06 canis fami
21	7	1.8	230	CLD2_HUMAN	P57739 homo sapien
22	7	1.8	272	MSA2_PLAF7	P50498 plasmodium
23	7	1.8	275	Y0JG_BACSU	P54544 bacillus su
24	7	1.8	284	SMX5_SCHMA	Q26604 schistosoma
25	7	1.8	286	SSRA_CANFA	P16967 canis fami
26	7	1.8	286	SSRA_HUMAN	P43307 homo sapien
27	7	1.8	286	SSRA_RABIT	P53815 oryctolagus
28	7	1.8	291	RGR_BOVIN	P47803 bos taurus
29	7	1.8	291	RGR_HUMAN	P47804 homo sapien
30	7	1.8	303	CAT2_HUMAN	O9ubt2 homo sapien
31	7	1.8	341	MOZ2_MOUSE	O06138 mus musculu
32	7	1.8	355	CHLI_NEPOL	O9108 nephrolepis
33	7	1.8	365	CYB_ASCSU	P24878 ascaris suu

34	7	1.8	373	1	YC08_KLEPN	Q48454 klebsiella
35	7	1.8	375	1	GDF8_CHICK	Q42220 gallus gall
36	7	1.8	375	1	GDF8_MERGA	Q42221 melagris g
37	7	1.8	377	1	MLC1_HUMAN	O15049 homo sapien
38	7	1.8	379	1	CYB_EQUUS	P92487 equus asinu
39	7	1.8	381	1	CYB_ANTNA	Q3800 antechinus
40	7	1.8	381	1	CYB_DASHA	Q34321 dasypus ha
41	7	1.8	381	1	CYB_NEOLO	Q35157 neophascoga
42	7	1.8	381	1	CYB_PHAEL	Q35409 phascogale
43	7	1.8	381	1	CYB_PHARA	Q35673 phascogale
44	7	1.8	381	1	CYB_PSEMO	Q35693 pseudantech
45	7	1.8	381	1	CYB_SMICR	Q35810 smilthopsis

ALIGNMENTS

RESULT 1
ID DAF_HUMAN STANDARD; PRT; 381 AA.
AC P08174; P09679; P78361;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Complement decay-accelerating factor precursor (CD55 antigen).
GN DAF OR CR OR CD55.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=87115845; PubMed=2433596;
RA Carras I.W., Davitz M.A., Rhee L., Wedgell G., Martin D.W. Jr.,
RA Nussenzweig V.,
RT "Cloning of decay-accelerating factor suggests novel use of splicing
RT to generate two proteins."
RL Nature 325:545-549(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 6-381 FROM N.A. (ISOFORM 2).
RX MEDLINE=87175602; PubMed=2436222;
RA Medof M.E., Lublin D.M., Holers V.M., Ayers D.J., Getty R.R.,
RA Leykam J.F., Atkinson J.P., Tykocinski M.L.;
RT "Cloning and characterization of cDNAs encoding the complete sequence
RT of decay-accelerating factor of human complement."
RL Proc. Natl. Acad. Sci. U.S.A. 84:2007-2011(1987).
RN [4]
RP SEQUENCE OF 35-381 FROM N.A. (ISOFORM 2).
RC TISSUE=Hippocampus;
RA Kumar V.B., Hyung C., Nakra R., Walters M., Sasser T., Bernardo A.;
RT "Decay-acceleration factor (DAF; CD 55) in the brain of Alzheimer's
RT disease patients."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 1-100 FROM N.A.
RX MEDLINE=91271256; PubMed=1711208;
RA Ewlonu U.K., Ravi L., Medof M.E.;
RT "Characterization of the decay-accelerating factor gene promoter
RT region."
RL Proc. Natl. Acad. Sci. U.S.A. 88:4675-4679(1991).
RN [6]
RP SEQUENCE OF 35-46.
RC TISSUE=Urine;
RX MEDLINE=91291869; PubMed=1712233;
RA Nakano Y., Sugita Y., Ishikawa Y., Choi N.-H., Tobe T., Tomita M.;
RT "Isolation of two forms of decay-accelerating factor (DAF) from human
RT urine."
RL Biochim. Biophys. Acta 1074:326-330(1991).

RN [7]
 RP GPI-ANCHOR.
 RX MEDLINE-91093238; PubMed-1824699;
 RA Moran P., Raab H., Kohr W.J., Carras I.W.;
 RT "Glycophospholipid membrane anchor attachment. Molecular analysis of
 the cleavage/attachment site.";
 RL J. Biol. Chem. 266:1250-1257(1991).
 RN [8]
 RP DISULFIDE BONDS IN SUSHI DOMAINS.
 RX MEDLINE-92305034; PubMed-1377029;
 RA Nakano Y., Sumida K., Kikuta N., Mura N.-H., Tobe T., Tomita M.;
 RT Complete determination of disulfide bonds localized within the short
 consensus repeat units of decay accelerating factor (CD55 antigen).";
 RL Biochim. Biophys. Acta 1116:235-240(1992).
 RN [9]
 RP FUNCTION AS A ECHOVIRUS RECEPTOR.
 RX MEDLINE-95045399; PubMed-7523274;
 RA Ward T., Pipkin P.A., Clarkson N.A., Stone D.M., Minor P.D.,
 RT "Decay-accelerating factor CD55 is identified as the receptor for
 echovirus 7 using FcR2s, a rapid immuno-focal cloning method.";
 RL EMBO J. 13:5070-5074(1994).
 RN [10]
 RP VARIANT BLOOD GROUP DR(A-).
 RX MEDLINE-94325573; PubMed-7519480;
 RA Lublin D.M., Mallinson G., Poole J., Reid M.E., Thompson E.S.,
 RT Ferdinand B.R., Telen M.J., Anstee D.J., Tanner M.J.A.;
 RT "Molecular basis of reduced or absent expression of
 decay-accelerating factor in Cromer blood group phenotypes.";
 RL Blood 84:1276-1282(1994).
 CC -1- FUNCTION: THIS PROTEIN RECOGNIZES C4B AND C3B FRAGMENTS THAT
 CONDENSE WITH CELL-SURFACE HYDROXYL OR AMINO GROUPS WHEN NASCENT
 C4B AND C3B ARE LOCALLY GENERATED DURING C4 AND C3 ACTIVATION.
 INTERACTION OF DAF WITH CELL-ASSOCIATED C4B AND C3B POLYPEPTIDES
 INTERFERES WITH THEIR ABILITY TO CATALYZE THE CONVERSION OF C2 AND
 FACTOR B TO ENZYMATICALLY ACTIVE C2A AND BB AND THEREBY PREVENTS
 THE FORMATION OF C4B2A AND C3BBB, THE AMPLIFICATION CONVERTASES OF
 THE COMPLEMENT CASCADE.
 CC -1- FUNCTION: ALSO ACTS AS THE RECEPTOR FOR ECHOVIRUS 7 AND RELATED
 VIRUSES (ECHOVIRUSES 13, 21, 29 AND 33).
 CC -1- SUBUNIT: MONOMER (MAJOR FORM) AND NON-DISULFIDE-LINKED, COVALENT
 HOMODIMER (MINOR FORM).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1/DAF-1 AND 2/DAF-2 (SHOWN
 HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE PLASMA MEMBRANES OF ALL CELL
 TYPES THAT ARE IN INTIMATE CONTACT WITH PLASMA MEMBRANES OF ALL CELL
 PROTEINS. IT IS ALSO FOUND ON THE SURFACES OF EPITHELIAL CELLS
 LINING EXTRACELLULAR COMPARTMENTS, AND VARIANTS OF THE MOLECULE
 ARE PRESENT IN BODY FLUIDS AND IN EXTRACELLULAR MATRIX.
 CC -1- DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR
 FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE
 ACTIVE SITE ON SCR3 (BY SIMILARITY).
 CC -1- PTM: THE SER/THR-RICH DOMAIN IS HEAVILY O-GLYCOSYLATED.
 CC -1- POLYMORPHISM: DAF IS RESPONSIBLE FOR THE CROMER BLOOD GROUP
 SYSTEM. IT CONSISTS OF AT LEAST SEVEN HIGH-INCIDENCE (CRA),
 TC(A), DR(A), ES(A), MES(B), UMC, AND IIC) AND LOW-INCIDENCE
 (TC(B), TC(C), AND MES(A)) ANTIGENS THAT RESIDE ON DAF. IN THE
 CROMER PHENOTYPES DR(A-) AND INAB THERE IS REDUCED OR ABSENT
 EXPRESSION OF DAF, RESPECTIVELY. IN THE CASE OF THE DR(A-)
 PHENOTYPE, A SINGLE NUCLEOTIDE SUBSTITUTION WITHIN EXON 5 ACCOUNTS
 FOR TWO CHANGES: A SIMPLE AMINO ACID SUBSTITUTION THAT IS THE
 BASIS OF THE ANTIGENIC VARIATION, AND AN ALTERNATIVE SPLICING
 EVENT THAT UNDERLIES THE DECREASED EXPRESSION OF DAF IN THIS
 PHENOTYPE.
 CC -1- SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
 (RCA) FAMILY.
 CC -1- DATABASE: NAME-PROW: NOTE=CD guide CD55 entry;
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd55.htm".
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M31516; AA52169.1; -;
 DR EMBL: M30142; AA52168.1; -;
 DR EMBL: BC001288; AAH01288.1; -;
 DR EMBL: M15799; AA52167.1; -;
 DR EMBL: U08576; AA548622.1; -;
 DR EMBL: M64653; AA52170.1; -;
 DR EMBL: M64356; AA52170.1; JOINED.
 DR EMBL: S72858; AAC60633.1; -;
 DR PIR: B26359; B26359.
 DR PIR: A26359; A26359.
 DR PIR: S16187; S16187.
 DR PIR: A39101; A39101.
 DR PIR: S23138; S23138.
 DR HSSP: P08603; 1HCC.
 DR Genew: HGNC:2665; DAF.
 DR MIM: 125240; -;
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF000084; sushi; 8.
 DR SMART: SM00032; CCP; 4.
 KW Complement pathway; Plasma; Glycoprotein; Membrane; Repeat;
 KW Alternative splicing; GPI-anchor; Signal; Polymorphism;
 KW Blood group antigen.
 FT SIGNAL 1 34
 FT CHAIN 35 353
 FT PROP 354 381
 FT DOMAIN 35 35
 FT DOMAIN 97 159
 FT DOMAIN 162 221
 FT DOMAIN 224 284
 FT DOMAIN 287 356
 FT DISULFID 36 81
 FT DISULFID 65 94
 FT DISULFID 98 145
 FT DISULFID 129 158
 FT DISULFID 163 204
 FT DISULFID 190 220
 FT DISULFID 225 267
 FT DISULFID 253 283
 FT CARBOHYD 95 95
 FT LIPID 353 353
 FT VARSPIC 362 381
 FT VARIANT 52 52
 FT VARIANT 52 52
 FT VARIANT 82 82
 FT VARIANT 199 199
 FT VARIANT 227 227
 FT CONFLICT 80 80
 FT CONFLICT 85 85
 FT CONFLICT 187 187
 FT CONFLICT 297 297
 SQ SEQUENCE 381 AA; 41388 MW; 29138EBB64B565E CRC64;
 Query Match 79.0%; Score 301; DB 1; Length 381;
 Best Local Similarity 100.0%; Pred. No. 1,4e-286; Indels 0; Gaps 0;
 Matches 301; Conservative 0; Mismatches 0;
 QY 81 CLKGSQMSDIEFCNCRSCVPTRLNSASLSKQPYITONTYPVGTVEYECRPGYRREPSSLS 140
 DB 81 CLKGSQMSDIEFCNCRSCVPTRLNSASLSKQPYITONTYPVGTVEYECRPGYRREPSSLS 140

QY 141 PKLCLONLWKSTAVECKKSCNPGCIRNGQIDVPGILFGATISPSCTGKLGEST 200
 DB 141 PKLCLONLWKSTAVECKKSCNPGCIRNGQIDVPGILFGATISPSCTGKLGEST 200
 QY 201 SSFLIGSSSVQWSDPLPECREITCPAPOLDNGIGERDHYGROSVTACKNGFM 260
 DB 201 SSFLIGSSSVQWSDPLPECREITCPAPOLDNGIGERDHYGROSVTACKNGFM 260
 QY 261 GHSIYCTVNNDEGEWSPPECKRGLSKVPTVQKPTVNVPTTEVSPTSOKTTKT 320
 DB 261 GHSIYCTVNNDEGEWSPPECKRGLSKVPTVQKPTVNVPTTEVSPTSOKTTKT 320
 QY 321 TTPNAQATRSYSPVSRTHKHEHTTPNKGSGTSGTTRLLSGHCPPLTGLGLVTMGL 380
 DB 321 TTPNAQATRSYSPVSRTHKHEHTTPNKGSGTSGTTRLLSGHCPPLTGLGLVTMGL 380
 QY 381 T 381
 DB 381 T 381

RESULT 2

DAF_PONPY STANDARD; PRT; 340 AA.

AC P49457;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Complement decay-accelerating factor (CD55) (Fragment).
 GN DAF OR CD55.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
 OX NCBI_TaxID=9600.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94110622; PubMed=7506731;
 RA Nickells M.W., Alvarez J.I., Lublin D.M., Atkinson J.P.;
 RT "Characterization of DAF-2, a high molecular weight form of decay-
 accelerating factor (DAF, CD55), as a covalently cross-linked dimer
 of DAF-1.";
 RT J. Immunol. 152:676-685(1994).

RL J. Immunol. 152:676-685(1994).
 CC -1- FUNCTION: THIS PROTEIN RECOGNIZES C4B AND C3B FRAGMENTS THAT
 CONDENSE WITH CELL-SURFACE HYDROXYL OR AMINO GROUPS WHEN NASCENT
 C4B AND C3B ARE LOCALLY GENERATED DURING C4 AND C3 ACTIVATION.
 CC INTERACTION OF DAF WITH CELL-ASSOCIATED C4B AND C3B POLYPEPTIDES
 INTERFERES WITH THEIR ABILITY TO CATALYZE THE CONVERSION OF C2 AND
 FACTOR B TO ENZYMATICALLY ACTIVE C2A AND BB AND THEREBY PREVENTS
 THE FORMATION OF C4B2A AND C3BB, THE AMPLIFICATION CONVERTASES OF
 THE COMPLEMENT CASCADE (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER (MAJOR FORM) AND NON-DISULFIDE-LINKED, COVALENT
 HOMODIMER (MINOR FORM).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; DAF-1 and DAF-2 (shown here);
 CC are produced by alternative splicing.
 CC -1- DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR
 FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE
 ACTIVE SITE ON SCR3 (BY SIMILARITY).
 CC -1- PTM: THE SER/THR-RICH DOMAIN IS HEAVILY O-GLYCOSYLATED.
 CC -1- SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
 (RCA) FAMILY.

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CC EMBL; S67775; AAC60609.1; -;
 DR HSSP; P08603; IAFI.

DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00084; sushi; 4.
 DR SMART; SM00032; CCP; 4.
 KW Complement pathway; Plasma; Glycoprotein; Membrane; Repeat;
 KW Alternative splicing; GPI-anchor; Sushi.

FT NON_TER 1
 FT CHAIN 1
 FT PROPEP 313 340 COMPLEMENT DECAY-ACCELERATING FACTOR.
 FT DOMAIN <1 54 SUSHI 1.
 FT DOMAIN 56 118 SUSHI 2.
 FT DOMAIN 121 180 SUSHI 3.
 FT DOMAIN 183 243 SUSHI 4.
 FT DOMAIN 246 315 SER/THR-RICH.
 FT DISULFID 24 53 BY SIMILARITY.
 FT DISULFID 57 104 BY SIMILARITY.
 FT DISULFID 88 117 BY SIMILARITY.
 FT DISULFID 122 163 BY SIMILARITY.
 FT DISULFID 149 179 BY SIMILARITY.
 FT DISULFID 184 226 BY SIMILARITY.
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT LIPID 107 107 GPI-ANCHOR (BY SIMILARITY).
 FT SEQUENCE 340 AA; 37180 MW; D3D865C058204290 CRC64;

Query Match 22.3%; Score 85; DB 1; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2, 5e-75;
 Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 DEGEWSPPECKRGLSKVPTVQKPTVNVPTTEVSPTSOKTTKTTPNAQATRS 331
 DB 231 DEGEWSPPECKRGLSKVPTVQKPTVNVPTTEVSPTSOKTTKTTPNAQATRS 290
 QY 332 PVSRTTKHHEHTTPNKGSGTSGTT 356
 DB 291 PVSRTTKHHEHTTPNKGSGTSGTT 315

RESULT 3

DAF_CAVPO STANDARD; PRT; 507 AA.

AC Q60401; Q60402; Q60403; Q60404; Q60405; Q60406; P97254; P97255;
 AC P97256; Q9WRT19;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Complement decay-accelerating factor precursor.
 GN DAF.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
 OX NCBI_TaxID=10141.
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

RC STRAIN-Hartley; TISSUE-Spleen;
 RX MEDLINE=95403978; PubMed=7545710;
 RA Nonaka M., Miwa T., Okada N., Nonaka M., Okada H.;
 RT "Multiple isoforms of guinea pig decay-accelerating factor (DAF)
 generated by alternative splicing.";
 RL J. Immunol. 155:3037-3048(1995).

CC -1- FUNCTION: PREVENTS THE FORMATION AND/OR ACCELERATES THE
 DISSOCIATION OF C3 CONVERTASE.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
 (ISOFORM 3); SECRETED (ISOFORMS 4).
 CC -1- ALTERNATIVE PRODUCTS: At least 7 isoforms; 1 (shown here), 2/GDA-
 TCS, 3/GDAB-GPI, 4/GDAB-SEC, 5/GDAB-TCL, 6/GDAB-TCL and 7/GDAB-
 TCS; are produced by alternative splicing. GDAB-SEC is the
 secreted form, GDAB-TCL and GDAB-TCL have a longer cytoplasmic
 region, GDA-TCS and GDAB-TCS have a shorter cytoplasmic region and
 GDAB-GPI is the GPI-anchored form.
 CC -1- TISSUE SPECIFICITY: ALL THE ISOFORMS ARE WIDELY EXPRESSED. GPI AND
 TCS ARE THE MAJOR FORMS, WHEREAS SEC IS MINOR AND TCL IS ONLY
 PRESENT IN TRACE LEVELS.

CC	-1- SIMILARITY: CONTAINS 4 SUSLI (SCR) DOMAINS.
CC	-1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
CC	(RCA) FAMILY.
CC	-----
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CC	-----
DR	EMBL; D55667; BAA09514.1; -
DR	EMBL; D55656; BAA09514.1; JOINED.
DR	EMBL; D55667; BAA09514.1; JOINED.
DR	EMBL; D55658; BAA09514.1; JOINED.
DR	EMBL; D55659; BAA09514.1; JOINED.
DR	EMBL; D55660; BAA09514.1; JOINED.
DR	EMBL; D55661; BAA09514.1; JOINED.
DR	EMBL; D55662; BAA09514.1; JOINED.
DR	EMBL; D55663; BAA09514.1; JOINED.
DR	EMBL; D55664; BAA09514.1; JOINED.
DR	EMBL; D55665; BAA09515.1; JOINED.
DR	EMBL; D55666; BAA09515.1; JOINED.
DR	EMBL; D55667; BAA09515.1; JOINED.
DR	EMBL; D55668; BAA09515.1; JOINED.
DR	EMBL; D55669; BAA09515.1; JOINED.
DR	EMBL; D55670; BAA09515.1; JOINED.
DR	EMBL; D55671; BAA09515.1; JOINED.
DR	EMBL; D55672; BAA09515.1; JOINED.
DR	EMBL; D55673; BAA09514.1; JOINED.
DR	EMBL; D55674; BAA09514.1; JOINED.
DR	EMBL; D55675; BAA09515.1; JOINED.
DR	EMBL; D55676; BAA09515.1; JOINED.
DR	EMBL; D55677; BAA09516.1; JOINED.
DR	EMBL; D55678; BAA09516.1; JOINED.
DR	EMBL; D55679; BAA09516.1; JOINED.
DR	EMBL; D55680; BAA09516.1; JOINED.
DR	EMBL; D55681; BAA09516.1; JOINED.
DR	EMBL; D55682; BAA09516.1; JOINED.
DR	EMBL; D55683; BAA09516.1; JOINED.
DR	EMBL; D55684; BAA09516.1; JOINED.
DR	EMBL; D55685; BAA09516.1; JOINED.
DR	EMBL; D55686; BAA09516.1; JOINED.
DR	EMBL; D55687; BAA09517.1; JOINED.
DR	EMBL; D55688; BAA09517.1; JOINED.
DR	EMBL; D55689; BAA09517.1; JOINED.
DR	EMBL; D55690; BAA09517.1; JOINED.
DR	EMBL; D55691; BAA09517.1; JOINED.
DR	EMBL; D55692; BAA09517.1; JOINED.
DR	EMBL; D55693; BAA09517.1; JOINED.
DR	EMBL; D55694; BAA09517.1; JOINED.
DR	EMBL; D55695; BAA09517.1; JOINED.
DR	EMBL; D55696; BAA09517.1; JOINED.
DR	EMBL; D55697; BAA09518.1; JOINED.
DR	EMBL; D55698; BAA09518.1; JOINED.
DR	EMBL; D55699; BAA09518.1; JOINED.
DR	EMBL; D55700; BAA09518.1; JOINED.
DR	EMBL; D55701; BAA09518.1; JOINED.
DR	EMBL; D55702; BAA09518.1; JOINED.
DR	EMBL; D55703; BAA09518.1; JOINED.
DR	EMBL; D55704; BAA09518.1; JOINED.
DR	EMBL; D55705; BAA09518.1; JOINED.
DR	EMBL; D55706; BAA09518.1; JOINED.
DR	EMBL; D55707; BAA09518.1; JOINED.
DR	EMBL; D55708; BAA09518.1; JOINED.
DR	EMBL; D55709; BAA09518.1; JOINED.
DR	EMBL; D55710; BAA09518.1; JOINED.
DR	EMBL; D55711; BAA09518.1; JOINED.
DR	EMBL; D55712; BAA09518.1; JOINED.
DR	EMBL; D55713; BAA09518.1; JOINED.
DR	EMBL; D55714; BAA09518.1; JOINED.
DR	EMBL; D55715; BAA09518.1; JOINED.
DR	EMBL; D55716; BAA09518.1; JOINED.
DR	EMBL; D55717; BAA09518.1; JOINED.
DR	EMBL; D55718; BAA09518.1; JOINED.
DR	EMBL; D55719; BAA09518.1; JOINED.
DR	EMBL; D55720; BAA09518.1; JOINED.
DR	EMBL; D55721; BAA09518.1; JOINED.
DR	EMBL; D55722; BAA09518.1; JOINED.
DR	EMBL; D55723; BAA09518.1; JOINED.
DR	EMBL; D55724; BAA09518.1; JOINED.
DR	EMBL; D55725; BAA09518.1; JOINED.
DR	EMBL; D55726; BAA09518.1; JOINED.
DR	EMBL; D55727; BAA09518.1; JOINED.
DR	EMBL; D55728; BAA09518.1; JOINED.
DR	EMBL; D55729; BAA09518.1; JOINED.
DR	EMBL; D55730; BAA09518.1; JOINED.
DR	EMBL; D55731; BAA09518.1; JOINED.
DR	EMBL; D55732; BAA09518.1; JOINED.
DR	EMBL; D55733; BAA09518.1; JOINED.
DR	EMBL; D55734; BAA09518.1; JOINED.
DR	EMBL; D55735; BAA09518.1; JOINED.
DR	EMBL; D55736; BAA09518.1; JOINED.
DR	EMBL; D55737; BAA09518.1; JOINED.
DR	EMBL; D55738; BAA09518.1; JOINED.
DR	EMBL; D55739; BAA09518.1; JOINED.
DR	EMBL; D55740; BAA09518.1; JOINED.
DR	EMBL; D55741; BAA09518.1; JOINED.
DR	EMBL; D55742; BAA09518.1; JOINED.
DR	EMBL; D55743; BAA09518.1; JOINED.
DR	EMBL; D55744; BAA09518.1; JOINED.
DR	EMBL; D55745; BAA09518.1; JOINED.
DR	EMBL; D55746; BAA09518.1; JOINED.
DR	EMBL; D55747; BAA09518.1; JOINED.
DR	EMBL; D55748; BAA09518.1; JOINED.
DR	EMBL; D55749; BAA09518.1; JOINED.

DR	EMBL:	D55660;	BAA09519.1;	JOINED.
DR	EMBL:	D55661;	BAA09519.1;	JOINED.
DR	EMBL:	D55662;	BAA09519.1;	JOINED.
DR	EMBL:	D55663;	BAA09519.1;	JOINED.
DR	EMBL:	D55664;	BAA09519.1;	JOINED.
DR	EMBL:	D55665;	BAA09519.1;	JOINED.
DR	EMBL:	D49416;	BAA08396.1;	-
DR	EMBL:	D49417;	BAA08397.1;	-
DR	EMBL:	D49418;	BAA08398.1;	-
DR	EMBL:	D49419;	BAA08399.1;	-
DR	EMBL:	D49420;	BAA08400.1;	-
DR	EMBL:	D49421;	BAA08401.1;	-
DR	InterPro:	IPR000436;	Sushi1_SCR_CCP.	
KM	Pfam:	PF00084;	sushi; 4.	
KW	Complement pathway: Glycoprotein; Membrane; Repeat; GPI-anchor;			
FT	Altenative splicing:	Signal:	Sushi.	POTENTIAL.
FT	SIGNAL	1	31	
FT	CHAIN	32	431	
FT	PROPEP	452	507	COMPLEMENT DECAT-ACCELERATING FACTOR.
FT	DOMAIN	32	93	REMOVED IN NATURE FORM (BY SIMILARITY).
FT	DOMAIN	94	158	SUSHI 1.
FT	DOMAIN	159	220	SUSHI 2.
FT	DOMAIN	221	283	SUSHI 3.
FT	DOMAIN	284	458	SUSHI 4.
FT	DOMAIN	284	458	SER/THR-RICH.
FT	DISULFID	33	80	BY SIMILARITY.
FT	DISULFID	64	92	BY SIMILARITY.
FT	DISULFID	96	144	BY SIMILARITY.
FT	DISULFID	127	157	BY SIMILARITY.
FT	DISULFID	162	203	BY SIMILARITY.
FT	DISULFID	189	219	BY SIMILARITY.
FT	DISULFID	224	266	BY SIMILARITY.
FT	LIPID	252	282	BY SIMILARITY.
FT	CARBOHYD	451	451	GPI-ANCHOR (BY SIMILARITY).
FT	CARBOHYD	57	57	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	93	93	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	174	174	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	442	442	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	493	493	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	302	334	MISSTNG (IN ISOFORM 2).
FT	VARSPLIC	335	366	MISSTNG (IN ISOFORM 2), ISOFORM 3, ISOFORM 4, ISOFORM 5 AND ISOFORM 7).
FT	VARSPLIC	399	424	MISSTNG (IN ISOFORM 3 AND ISOFORM 4).
FT	VARSPLIC	455	458	MISSTNG (IN ISOFORM 3, ISOFORM 4, ISOFORM 5 AND ISOFORM 6).
FT	VARSPLIC	459	507	THYRVDSFCAGASHMWLADIKEDLRDFESNAQNISSILQ VLGAAQTQ -> GHMCIKTLVLLVVIIG (IN ISOFORM 3).
FT	VARSPLIC	459	507	THYRVDSFCAGASHMWLADIKEDLRDFESNAQNISSILQ VLGAAQTQ -> DHNVC (IN ISOFORM 4).
FT	VARSPLIC	459	507	THYRVDSFCAGASHMWLADIKEDLRDFESNAQNISSILQ VLGAAQTQ -> ANNRRHMTKNPMLVYT (IN ISOFORM 2 AND ISOFORM 7).
FT	SEQUENCE	507 AA;	55263 MW;	D25BBB749425210 CRC64;
Query Match	Best Local Similarity	3.4%;	Score 13;	DB 1;
Matches	13;	Conservative	100.0%;	Pred. No. 9.5e-05;
OY	89	DIEEFCNRSCVP	101	Mismatches 0;
ID	87	DIEEFCNRSCVP	99	Indels 0;
RESULT 4				
DAFI_MOUSE				
AC	061475;	061397;	p97732;	PRT;
DT	01-NOV-1997	(Rel. 35;	Created)	390 AA.
DT	01-NOV-1997	(Rel. 35;	Last sequence update)	
DT	13-JUL-1999	(Rel. 38;	Last annotation update)	
DE	Complement decay-accelerating factor, GPI-anchored precursor (DAF-GPI).			
GN	DAFI.			

OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=95403982; Pubmed=7545711;
 RA Spicer A.P., Seldin M.F., Gendler S.J.;
 RT "Molecular cloning and chromosomal localization of the mouse decay-
 RT accelerating factor genes. Duplicated genes encode
 RT glycosylphosphatidylinositol-anchored and transmembrane forms.";
 RL J. Immunol. 155:3079-3091(1995).
 RN [2]
 RP SEQUENCE OF 7-390 FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Spleen;
 RX MEDLINE=96362213; Pubmed=8671624;
 RA Fukuda Y., Yasui A., Okada N., Okada H.;
 RT "Immunoscreening."
 RT Int. Immunol. 8:379-385(1996).
 CC -1- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- TISSUE SPECIFICITY: BRAIN, SECRETORY EPITHELIA, SKELETAL MUSCLE,
 CC LIVER, TESTES, THYMUS, SPLEEN AND LYMPH NODE.
 CC -1- DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR
 CC FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE
 CC ACTIVE SITE ON SCR3 (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
 CC (RCA) FAMILY.
 CC -----
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 CC -----
 DR EMBL: LA1366; AAB00092.1; -;
 DR EMBL: D63679; BAA09830.1; -;
 DR HSSP: P08603; IHCC.
 DR MGD: MGI:104850; Daf1.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00084; sushi. 4.
 DR SMART: SM00032; CCP; 4.
 KW Complement pathway; Glycoprotein; Membrane; Repeat; GPI-anchor;
 KW Signal; Sushi.
 FT SIGNAL 1 34
 FT CHAIN 35 361
 FT PROPER 362 390
 FT DOMAIN 35 95
 FT DOMAIN 97 159
 FT DOMAIN 162 221
 FT DOMAIN 224 285
 FT DOMAIN 288 364
 FT DISULFID 65 94
 FT DISULFID 98 145
 FT DISULFID 129 158
 FT DISULFID 163 204
 FT DISULFID 190 220
 FT DISULFID 225 267
 FT DISULFID 253 284
 FT CARBOHYD 187 187
 FT CARBOHYD 262 262
 FT LIPID 361 361
 FT CONFLICT 9 7
 FT CONFLICT 83 9
 FT CONFLICT 91 91
 E -> G (IN REF. 2).
 FT CONFLICT 91

FT CONFLICT 135 135 E -> K (IN REF. 2).
 FT CONFLICT 173 173 H -> L (IN REF. 2).
 FT CONFLICT 180 180 I -> T (IN REF. 2).
 SQ SEQUENCE 390 AA; 42618 MW; 4418721DFF47F8E7 CRC64;
 Query Match 2.68; Score 10; DB 1; Length 390;
 Best Local Similarity 100.0%; Pred. No. 0.065;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 157 FCKRKSQNP 166
 DB 157 FCKRKSQNP 166
 RESULT 5
 DAF2_MOUSE
 ID DAF2_MOUSE STANDARD; PRT; 407 AA.
 AC 061476;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Complement decay-accelerating factor, transmembrane precursor
 DE (DAF-TM).
 GN DAF2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=95403982; Pubmed=7545711;
 RA Spicer A.P., Seldin M.F., Gendler S.J.;
 RT "Molecular cloning and chromosomal localization of the mouse decay-
 RT accelerating factor genes. Duplicated genes encode
 RT glycosylphosphatidylinositol-anchored and transmembrane forms.";
 RL J. Immunol. 155:3079-3091(1995).
 CC -1- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: TESTIS, SPLEEN AND LYMPH NODE.
 CC -1- DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR
 CC FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE
 CC ACTIVE SITE ON SCR3 (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
 CC (RCA) FAMILY.
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 CC -----
 DR EMBL: LA1365; AAB00092.1; -;
 DR HSSP: P08603; IHCC.
 DR MGD: MGI:104849; Daf2.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00084; sushi. 4.
 DR SMART: SM00032; CCP; 4.
 KW Complement pathway; Glycoprotein; Repeat; Signal; Sushi;
 KW Transmembrane.
 FT SIGNAL 1 39
 FT CHAIN 40 407
 FT DOMAIN 40 368
 FT TRANSMEM 369 389
 FT DOMAIN 390 407
 FT DOMAIN 40 100
 FT DOMAIN 102 164
 FT DOMAIN 167 226
 SUSHI 1.
 SUSHI 2.
 SUSHI 3.

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FT DOMAIN 229 SUSHI 4.
FT DOMAIN 291 SER/THR-RICH (BY SIMILARITY).
FT DISULFID 70 363
FT DISULFID 103 99 BY SIMILARITY.
FT DISULFID 134 150 BY SIMILARITY.
FT DISULFID 168 163 BY SIMILARITY.
FT DISULFID 195 209 BY SIMILARITY.
FT DISULFID 230 225 BY SIMILARITY.
FT DISULFID 258 272 BY SIMILARITY.
FT CARBOHYD 192 285 BY SIMILARITY.
FT CARBOHYD 267 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 407 AA: 44469 MW: DDD82FD72CEAD40 CRC64;

Query Match 2.6%; Score 10; DB 1; Length 407;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 FCKKSCPNP 166
DB 162 FCKKSCPNP 171

RESULT 6
APOH_HUMAN STANDARD: PRT: 345 AA.
ID APOH_HUMAN P02749:
AC 21-JUL-1986 (Rel. 01, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)
DE (Beta(2)GPI) (Activated protein C-binding protein) (APC inhibitor).
GN APOH OR B2GI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91315408; PubMed=1650181;
RA Steinkasserer A., Estaller C., Weiss E., Sim R.B., Day A.J.;
RT "Complete nucleotide and deduced amino acid sequence of human beta 2-
RT glycoprotein I.";
RL Biochem. J. 277:387-391(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92008618; PubMed=1655523;
RA Kristensen T., Schousboe I., Boel E., Mulvihill E.M., Hansen R.R.,
RT Moeller K.B., Moeller N.P.H., Sottrup-Jensen L.;
RT "Molecular cloning and mammalian expression of human beta
RT 2-glycoprotein I cDNA.";
RL FEBS Lett. 289:183-186(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92084151; PubMed=1748314;
RA Mehdi H., Nunn M., Steel D.M., Whitehead A.S., Perez M., Walker L.,
RT Peebles M.E.;
RT "Nucleotide sequence and expression of the human gene encoding
RT apolipoprotein H (beta 2-glycoprotein I).";
RL Gene 108:293-298(1991).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92273779; PubMed=1339416;
RA Day J.R., O'Hara P.J., Grant F.J., Lofton-Day C.E., Berkaw M.N.,
RT Werner P., Arnard P.;
RT "Molecular cloning and sequence analysis of the cDNA encoding human
RT apolipoprotein H (beta 2-glycoprotein I).";
RL Int. J. Clin. Lab. Res. 21:256-263(1992).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=92135065; PubMed=1777418;
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RA Matsura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K.,
RA Tasada T., Koike T.;
RT "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by
RT cDNA cloning and inter-species differences of beta 2-GPI in
RT alternation of anticardiolipin binding.";
RL Int. Immunol. 3:1217-1221(1991).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=99115472; PubMed=9914524;
RA Okkels H., Rasmussen T.E., Sanghera D.K., Kamboh M.I., Kristensen T.;
RT "Structure of the human beta2-glycoprotein I (apolipoprotein H)
RT gene.";
RL Eur. J. Biochem. 259:435-440(1999).
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 20-345, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=84222015; PubMed=6587378;
RA Lozier J., Takahashi N., Putnam F.W.;
RT "Complete amino acid sequence of human plasma beta 2-glycoprotein I.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3640-3644(1984).
RN [9]
RP SEQUENCE OF 20-38.
RC TISSUE=Follicular fluid;
RX MEDLINE=21148139; PubMed=11250549;
RA Aleporou-Marinou V., Pappa H., Yalouris P., Patargias T.;
RT "Purification of apolipoprotein H (beta 2-glycoprotein I)-like protein
RT from human follicular fluid.";
RL Comp. Biochem. Physiol. 128B:537-542(2001).
RN [10]
RP DISULFIDE BONDS IN C-TERMINAL DOMAIN.
RX MEDLINE=93050249; PubMed=1426288;
RA Steinkasserer A., Barlow P.N., Willis A.C., Kertesz Z.,
RA Campbell I.D., Sim R.B., Norman D.G.;
RT "Activity, disulphide mapping and structural modelling of the fifth
RT domain of human beta 2-glycoprotein I.";
RL FEBS Lett. 313:193-197(1992).
RN [11]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=97299942; PubMed=915091;
RA Gambino R., Rulu G., Pagano G., Cassader M.;
RT "Qualitative analysis of the carbohydrate composition of
RT apolipoprotein H.";
RL J. Protein Chem. 16:205-212(1997).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RC TISSUE=Plasma;
RX MEDLINE=99437994; PubMed=10508150;
RA Bouna B., de Groot P.G., van Den Elsen J.M.H., Ravelli R.B.G.,
RA Schouten A., Simmelink M.J.A., Derksen R.H.W.M., Kroon J., Gros P.;
RT "Adhesion mechanism of human beta(2)-glycoprotein I to phospholipids
RT based on its crystal structure.";
RL EMBO J. 18:5166-5174(1999).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.87 ANGSTROMS).
RX MEDLINE=20031634; PubMed=10562535;
RA Schwarzenbacher R., Zeth K., Diederichs K., Gries A., Kostner G.M.,
RA Laggner P., Prassl R.;
RT "Crystal structure of human beta2-glycoprotein I: implications for
RT phospholipid binding and the antiphospholipid syndrome.";
RL EMBO J. 18:6228-6239(1999).
RN [14]
RP VARIANT LEU-266.
RX MEDLINE=93277313; PubMed=8099061;
RA Steinkasserer A., Doerner C., Wuerzner R., Sim R.B.;
RT "Human beta 2-glycoprotein I: molecular analysis of DNA and amino
RT acid polymorphism.";
RL Hum. Genet. 91:401-402(1993).
RN [15]
RP VARIANT ASN-107.
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RX MEDLINE-97369481; PubMed-9225969;
 RA Sanghera D.K., Kristensen T., Hamman R.F., Kamboh M.I.;
 RT "Molecular basis of the apolipoprotein H (beta 2-glycoprotein I)
 RT protein polymorphism";
 RL Hum. Genet. 100:57-62(1997).
 RN [16]
 RP VARIANTS GLY-325 AND SER-335.
 RX MEDLINE-97217791; PubMed-9063752;
 RA Sanghera D.K., Magenhecht D.R., McInyre J.A., Kamboh M.I.;
 RT "Identification of structural mutations in the fifth domain of
 RT apolipoprotein H (beta 2-glycoprotein I) which affect phospholipid
 RT binding.";
 RL Hum. Mol. Genet. 6:311-316(1997).
 CC -1- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES
 CC SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT
 CC ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING
 CC TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.
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 CC -----
 CC
 DR EMBL: X58100; CAA41113.1; -;
 DR EMBL: X53595; CAA37664.1; -;
 DR EMBL: X57847; CAA40977.1; -;
 DR EMBL: M62839; AAA51766.1; -;
 DR EMBL: S80305; AAB21330.1; -;
 DR EMBL: Y11493; CAA72279.1; -;
 DR EMBL: Y11494; CAA72279.1; JOINED.
 DR EMBL: Y11495; CAA72279.1; JOINED.
 DR EMBL: X53595; CAA72279.1; JOINED.
 DR EMBL: Y11496; CAA72279.1; JOINED.
 DR EMBL: Y11497; CAA72279.1; JOINED.
 DR EMBL: Y11498; CAA72279.1; JOINED.
 DR EMBL: Y17754; CAA72279.1; JOINED.
 DR EMBL: BC020703; AAH20703.1; -;
 DR PIR: S17178; NBHU.
 DR PIR: B43286; B43286.
 DR PDB: LOUB: 08-OCT-99.
 DR PDB: 1C12; 19-NOV-99.
 DR Genew; HSCN:616; APOH.
 DR MIM; 138700; -;
 DR InterPro: IPR000436; Sush1_SCR_CCP.
 DR Pfam: PF00084; sush1; 4.
 DR SMART: SM00032; CCP; 4.
 KW Heparin-binding; Glycoprotein; Plasma; Repeat; Sush1; Signal;
 KW Polymorphism; 3D-structure.
 FT STGNL 1 19
 FT CHAIN 20 345 BETA-2-GLYCOPROTEIN I.
 FT DOMAIN 22 80 SUSHI 1.
 FT DOMAIN 83 138 SUSHI 2.
 FT DOMAIN 141 201 SUSHI 3.
 FT DOMAIN 204 261 SUSHI 4.
 FT DOMAIN 263 345 SUSHI-LIKE.
 FT DISULFID 23 66
 FT DISULFID 51 79
 FT DISULFID 84 124
 FT DISULFID 110 137
 FT DISULFID 142 188
 FT DISULFID 174 200
 FT DISULFID 205 248
 FT DISULFID 234 260
 FT DISULFID 264 315
 FT DISULFID 300 325
 FT DISULFID 307 345
 FT CARBOHYD 149
 FT CARBOHYD 162
 O-LINKED.
 N-LINKED (GLCNAC. . .).

FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .).
 FT VARIANT 107 107 S -> N (IN APOH*1).
 FT /FTID=VAR_008169.
 Query Match 2.4%; Score 9; DB 1; Length 345;
 Best Local Similarity 100.0%; Pred. No. 0.56;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 185 TISFSCNTG 193
 Db 105 TISFSCNTG 113
 RESULT 7
 ID TAL_PSEAE STANDARD; PRT; 307 AA.
 AC Q91047;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Transaldolase (EC 2.2.1.2).
 GN TAL OR PA2796.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE-20437337; PubMed-10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garner R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen";
 RL Nature 406:959-964(2000).
 CC -1- FUNCTION: Transaldolase is important for the balance of
 CC metabolites in the pentose-phosphate pathway (by similarity).
 CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
 CC 3-phosphate -> D-erythrose 4-phosphate + D-fructose 6-phosphate.
 CC -1- PATHWAY: Pentose phosphate pathway; nonoxidative part.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY, SUBFAMILY 1.
 CC -----
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 CC -----
 CC
 DR EMBL: AE004707; AAC06184.1; -;
 DR HSSP; P30148; IONR.
 DR InterPro: IPR001585; Transaldolase.
 DR InterPro: IPR004730; Transaldolase_AB.
 DR Pfam: PF00923; Transaldolase; 1.
 DR TIGRPFAMs: TIGR00874; talAB; 1.
 DR PROSITE; PS01054; TRANSALDOLASE_1; 1.
 DR PROSITE; PS00958; TRANSALDOLASE_2; 1.
 KW Transferrase; Pentose shunt; Complete proteome.
 FT ACT SITE 125 125 BY SIMILARITY.
 SQ SEQUENCE 307 AA; 33946 MW; 840B2B6AF288594 CRC64;
 Query Match 2.1%; Score 8; DB 1; Length 307;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      16 GELPRLL 23
      1111111
DB      249 GELPRLL 256

RESULT 8
ASPG_DEIRA
ID      ASPG_DEIRA      STANDARD;      PRT;      322 AA.
AC      Q9RX9;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Probable L-asparaginase (EC 3.5.1.1) (L-asparagine amidohydrolase)
DE      (L-ASNase)
GN      ANSA OR DR2353.
OS      Deinococcus radiodurans.
OC      Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OX      Deinococcaceae; Deinococcus.
RN      NCBI_TaxID=1299;
RP      SEQUENCE FROM N.A.
RC      STRAIN=RI;
RA      MEDLINE=20036896; PubMed=10567266;
RA      White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA      Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA      Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA      Vamathevan J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA      Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischman R.D.,
RA      Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA      Fraser C.M.;
RT      "Genome sequence of the radioresistant bacterium Deinococcus
RT      radiodurans RI".
RL      Science 286:1571-1577(1999).
CC      -1- CATALYTIC ACTIVITY: L-asparagine + H(2)O = L-aspartate + NH(3).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC      -1- SIMILARITY: BELONGS TO THE ASPARAGINASE 1 FAMILY.
-----
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CC      or send an email to license@isb-sib.ch).
-----
CC      EMBL; AE002066; AAF11899.1; ALT_INIT.
CC      HSSP; P50286; IWSA.
DR      TIGR; DR2353; -.
DR      InterPro: IPR000267; Asp/Glutamase.
DR      Pfam; PF00710; Asparaginase; 1.
DR      PRINTS; PR00139; ASNGLNASE.
DR      ProDom; PD003221; Asp/Glutamase; 1.
DR      PROSITE; PS00144; ASN_GLNASE_1; 1.
DR      PROSITE; PS00917; ASN_GLNASE_2; FALSE_NEG.
KW      Hydrolyase; Complete proteome.
FT      ACT_SITE 16 16 BY SIMILARITY.
FT      ACT_SITE 87 87 BY SIMILARITY.
FT      ACT_SITE 88 88 BY SIMILARITY.
FT      ACT_SITE 158 158 BY SIMILARITY.
SQ      SEQUENCE 322 AA; 33806 MW; 0339A30B5A7E130E CRC64;

Query Match      2.1%; Score 8; DB 1; Length 322;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AC      P36897;
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      TGF-beta receptor type I precursor (EC 2.7.1.37) (TGFR-1) (TGF-beta
DE      type I receptor) (Serine/threonine-protein kinase receptor R4) (SKR4)
DE      (Activin receptor-like kinase 5) (ALK-5).
GN      TGFBR1.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=94061986; PubMed=8242743;
RA      Franzen P., ten Dijke P., Ichijo H., Yamashita H., Schulz P.,
RA      Heldin C.-H., Miyazono K.;
RT      "Cloning of a TGF beta type I receptor that forms a heteromeric
RT      complex with the TGF beta type II receptor."
RT      Cell 73:681-692(1993).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98086485; PubMed=9417915;
RA      Vellucci V.F., Reiss M.;
RT      "Cloning and genomic organization of the human transforming growth
RT      factor-beta type I receptor gene."
RT      Genomics 46:278-283(1997).
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Lynch M.A., Song H., Degroff V.L., Alam K.Y., Adams E.M.,
RA      Weghorst C.M.;
RT      "The genomic structure of the gene encoding the human transforming
RT      growth factor beta type I receptor."
RT      Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      3D-STRUCTURE MODELING OF 34-114.
RX      MEDLINE=96096781; PubMed=8521960;
RA      Jokiranta T.S., Tissari J., Teleman O., Merl S.;
RT      "Extracellular domain of type I receptor for transforming growth
RT      factor-beta: molecular modelling using protectin (CD59) as a
RT      template."
RT      FEBS Lett. 376:31-36(1995).
CC      -1- FUNCTION: TYPE I/TYPE II TGF-BETA RECEPTORS FORM AN HETEROERIC
CC      COMPLEX AFTER BINDING TGF-BETA AT THE CELL SURFACE AND ACT AS
CC      SIGNAL TRANSDUCERS.
CC      -1- CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- TISSUE SPECIFICITY: FOUND IN ALL TISSUES EXAMINED. MOST ABUNDANT
CC      IN PLACENTA AND LEAST ABUNDANT IN BRAIN AND HEART.
CC      -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC      TGF RECEPTOR SUBFAMILY.
-----
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-----
CC      EMBL; L11695; AAA16073.1; -.
DR      EMBL; AF054596; AAC08998.1; -.
DR      EMBL; AF054590; AAC08998.1; JOINED.
DR      EMBL; AF054591; AAC08998.1; JOINED.
DR      EMBL; AF054592; AAC08998.1; JOINED.
DR      EMBL; AF054593; AAC08998.1; JOINED.
DR      EMBL; AF054594; AAC08998.1; JOINED.
DR      EMBL; AF054595; AAC08998.1; JOINED.
DR      EMBL; AF054596; AAC08998.1; JOINED.
DR      EMBL; AF054597; AAC08998.1; JOINED.
DR      EMBL; AF035670; AAD02042.1; -.
DR      EMBL; AF035662; AAD02042.1; JOINED.
DR      EMBL; AF035663; AAD02042.1; JOINED.
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DR EMBL: AF035664; AAD02042.1; JOINED.
 DR EMBL: AF035665; AAD02042.1; JOINED.
 DR EMBL: AF035666; AAD02042.1; JOINED.
 DR EMBL: AF035667; AAD02042.1; JOINED.
 DR EMBL: AF035668; AAD02042.1; JOINED.
 DR EMBL: AF035669; AAD02042.1; JOINED.
 DR PDB: 1TBI; 08-NOV-96.
 DR Genew; HGNC:11772; TGFBR1.
 DR MIM: 190181; -.
 DR InterPro: IPR000472; Activin_rec.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF01064; Activin_rec; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00467; GS; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
 KM Transmembrane; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 503
 FT DOMAIN 25 125 TGF-BETA RECEPTOR TYPE I.
 FT TRANSMEM 126 147 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 148 503 POTENTIAL.
 FT BINDING 205 495 CYTOPLASMIC (POTENTIAL).
 FT NP_BIND 211 219 ATP (BY SIMILARITY).
 FT BINDING 232 232 ATP (BY SIMILARITY).
 FT ACT_SITE 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 36 54 BY SIMILARITY.
 FT DISULFID 38 41 BY SIMILARITY.
 FT DISULFID 48 71 BY SIMILARITY.
 FT DISULFID 86 100 BY SIMILARITY.
 FT DISULFID 101 106 BY SIMILARITY.
 SQ SEQUENCE 503 AA; 55959 MW; 179F11404725DDCB CRC64;

Query Match 2.1%; Score 8; DB 1; Length 503;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 19 PRLLLV 26
 Db 10 PRLLLV 17
 RESULT 10
 PME_PRUPE
 ID PME_PRUPE STANDARD; PRT; 522 AA.
 AC 043062;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Pectinesterase PPE8B precursor (EC 3.1.1.11) (Pectin methylsterase)
 DE (PE).
 OS Prunus persica (Peach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCBI_TaxID=3760;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Coronet; TISSUE=Fruit;
 RA Glover H., Brady C.J., Lee E., Speirs J.;
 RT "Multiple pectin esterase genes are expressed in ripening peach fruit:
 RT nucleotide sequence of a cDNA encoding peach pectin esterase.";
 RL (In) Plant Gene Register PG896-094.
 CC "-FUNCTION: MAY HAVE ROLES IN THE DEPOSITION OF PECTIN IN DEVELOPING
 CC TISSUES AND IN THE WALL LOOSENING AND CELL SEPARATION THAT OCCURS
 CC IN CELL EXPANSION, FRUIT RIPENING AND ABSCISSION."
 CC "- CATALYTIC ACTIVITY: Pectin + N H(2)O = N methanol + pectate.

CC -1- DEVELOPMENTAL STAGE: PRESENT THROUGHOUT FRUIT DEVELOPMENT.
 CC -1- SIMILARITY: BELONGS TO THE PECTINESTERASE FAMILY.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-6 IS THE INITIATOR.
 CC
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 CC
 DR EMBL: X95991; CAA65237.1; -.
 DR InterPro: IPR000070; Pectinesterase.
 DR Pfam: PF01095; Pectinesterase; 1.
 DR PROSITE: PS00800; PECTINESTERASE_1; 1.
 DR PROSITE: PS00503; PECTINESTERASE_2; 1.
 DR Signal; Hydrolase; Aspartyl esterase; Cell wall; Glycoprotein;
 KW Multigene family.
 FT SIGNAL 1 30
 FT CHAIN 31 522
 FT DOMAIN 253 256 POLY-LYS.
 FT ACT_SITE 336 336 BY SIMILARITY.
 FT ACT_SITE 357 357 BY SIMILARITY.
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 489 489 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 496 496 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 522 AA; 57396 MW; 6F9211A516C7949A CRC64;

Query Match 2.1%; Score 8; DB 1; Length 522;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 21 LLLLVLC 28
 Db 18 LLLLVLC 25
 RESULT 11
 UL25_HSV62
 ID UL25_HSV62 STANDARD; PRT; 555 AA.
 AC P52537;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Virion protein U50.
 DE U50 OR KAI1R.
 OS Human herpesvirus (type 6 / strain 229) (HHV6).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Roseolovirus.
 OX NCBI_TaxID=36351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95074921; Pubmed=7983761;
 RA Stamey F.R., Dominguez G., Black J.B., Dambaugh T.R., Pellett P.E.;
 RT "Intragenomic linear amplification of human herpesvirus 6B orlyt
 RT suggests acquisition of orlyt by transposition.";
 RL J. Virol. 69:589-596(1995).
 CC "-FUNCTION: VIRION PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
 CC EBV-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.
 CC
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CC  -----
DR  EMBL: AF157706; AAB06348.1; -.
DR  InterPro: IPR002493; UL25.
DR  Pfam: PF01499; UL25; 1.
SQ  SEQUENCE 555 AA; 63830 MW; 68B86590DC4CD2BC CRC64;

Query Match      2.1%; Score 8; DB 1; Length 555;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  71 KIPEKDS 78
Db  311 KIPEKDS 318

RESULT 12
CABP_RAT
ID  CABP_RAT      STANDARD;      PRT; 558 AA.
AC  063514;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  C4b-binding protein alpha chain precursor (C4bp).
GN  C4BPA.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Sprague-Dawley; TISSUE=Liver;
RX  MEDLINE=9716082; PubMed=9013975;
RA  Hillarp A., Wiklund H., Thern A., Dahlback B.;
RT  *Molecular cloning of rat C4b binding protein alpha- and beta-chains:
RT  structural and functional relationships among human, bovine, rabbit,
RT  mouse, and rat proteins.*;
RL  J. Immunol. 158:1315-1323(1997).
CC  -1- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT
CC  ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR
CC  (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT
CC  ALSO ACCELERATES THE DEGRADATION OF THE C4B2A COMPLEX (C3
CC  CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA
CC  CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S
CC  AND WITH SERUM AMYLOID P COMPONENT.
CC  -1- SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS.
CC  -1- SIMILARITY: TO C4BP BETA CHAIN AND TO PTG APOLIPOPROTEIN R.
CC  -1- SIMILARITY: CONTRAINS 8 SUSHI (SCR) DOMAINS.
CC  -----
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CC  -----
DR  EMBL: Z50051; CAA90391.1; -.
DR  HSSP: P10998; 1VD.
DR  InterPro: IPR000436; Sushi_SCR_CCP.
DR  Pfam: PF00084; sushi; 8.
DR  SMART: SM00032; CCP; 8.
KM  Complement pathway; Plasma; Glycoprotein; Repeat; Sushi; Signal.
FT  SIGNAL 1 13
FT  CHAIN 14 558 CAB-BINDING PROTEIN ALPHA CHAIN.
FT  DOMAIN 14 73 SUSHI 1.
FT  DOMAIN 76 135 SUSHI 2.
FT  DOMAIN 138 200 SUSHI 3.
FT  DOMAIN 203 259 SUSHI 4.
FT  DOMAIN 262 325 SUSHI 5.
FT  DOMAIN 328 387 SUSHI 6.
FT  DOMAIN 389 444 SUSHI 7.

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FT  DOMAIN 446 502 SUSHI 8.
FT  DISULFID 15 60 BY SIMILARITY.
FT  DISULFID 45 72 BY SIMILARITY.
FT  DISULFID 77 118 BY SIMILARITY.
FT  DISULFID 104 134 BY SIMILARITY.
FT  DISULFID 139 182 BY SIMILARITY.
FT  DISULFID 168 199 BY SIMILARITY.
FT  DISULFID 204 246 BY SIMILARITY.
FT  DISULFID 232 258 BY SIMILARITY.
FT  DISULFID 263 312 BY SIMILARITY.
FT  DISULFID 296 324 BY SIMILARITY.
FT  DISULFID 328 351 BY SIMILARITY.
FT  DISULFID 329 373 BY SIMILARITY.
FT  DISULFID 363 386 BY SIMILARITY.
FT  DISULFID 390 431 BY SIMILARITY.
FT  DISULFID 417 443 BY SIMILARITY.
FT  DISULFID 447 488 BY SIMILARITY.
FT  DISULFID 474 501 BY SIMILARITY.
FT  DISULFID 509 509 INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).
FT  DISULFID 521 521 INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).
FT  CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 469 469 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 491 491 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE 558 AA; 62266 MW; 592F0C667ED15FF CRC64;

Query Match      2.1%; Score 8; DB 1; Length 558;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  213 WSDPLEC 220
Db  127 WSDPLEC 134

RESULT 13
RS15_PSEPU
ID  RS15_PSEPU      STANDARD;      PRT; 89 AA.
AC  087791;
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DT  30-MAY-2000 (Rel. 39, Last annotation update)
DE  30S ribosomal protein S15.
GN  RPSO.
OS  Pseudomonas putida.
OC  Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC  Pseudomonas.
OX  NCBI_TaxID=303;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-TMB;
RA  Favaro R., Deno' G.;
RT  *Identification and cloning of genes involved in RNA turnover in
RT  Pseudomonas putida.*;
RL  Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
CC  -1- FUNCTION: THIS PROTEIN IS ONE OF THE 16S RIBOSOMAL RNA BINDING
CC  PROTEINS (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE S15P FAMILY OF RIBOSOMAL PROTEINS.
CC  -----
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CC  -----
DR  EMBL: Y18132; CAA7047.1; -.
DR  HSSP: P80378; 1AB3.
DR  InterPro: IPR005290; RS15_bact.
DR  InterPro: IPR000589; Ribosomal_S15.
DR  Pfam: PF00312; Ribosomal_S15; 1.

```

DR TIGR00952; S15_bact; 1.
 DR PROSITE; PS00362; RIBOSOMAL_S15; FALSE_NEG.
 KW Ribosomal protein; rRNA-binding.
 SQ SEQUENCE 89 AA; 9901 MW; 7CD73B1FE194EC4F CRC64;

Query Match 1.8%; Score 7; DB 1; Length 89;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 317 TTKTTP 323
 |||||
 Db 46 TTKTTP 52

RESULT 14
 B2MG_CEBAL STANDARD; PRT; 119 AA.
 AC 077826;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Beta-2-microglobulin precursor.
 GN B2M.
 OS Cebus albifrons (White-fronted capuchin),
 OS Cebus apella (Brown-capped capuchin), and
 OS Cebus olivaceus (Weeper capuchin).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
 OX NCBI_TaxID=9514, 9515, 37295;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=98298008; PubMed=9634477;
 RA Canavez F.C., Ladasky J.J., Muniz J.A.P.C., Seunarez H.N., Parham P.;
 RT "Beta-2-microglobulin in neotropical primates (Platyrrhini).";
 RL Immunogenetics 48:133-140(1998).
 CC -!- FUNCTION: BETA-2-MICROGLOBULIN IS THE BETA-CHAIN OF MAJOR
 CC HISTOCOMPATIBILITY COMPLEX CLASS I MOLECULES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
 CC -----
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 CC -----
 CC
 DR EMBL; AF032022; AAC39795.1; -;
 DR EMBL; AF032020; AAC39795.1; JOINED.
 DR EMBL; AF032021; AAC39795.1; JOINED.
 DR EMBL; AF031892; AAC39794.1; -;
 DR EMBL; AF031890; AAC39794.1; JOINED.
 DR EMBL; AF031891; AAC39794.1; JOINED.
 DR EMBL; AF032018; AAC52108.1; -;
 DR EMBL; AF032017; AAC52108.1; JOINED.
 DR HSSP; P01884; 1A6Z.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_C1.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00407; IgC1; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR MHC I; Signal; 1.
 FT SIGNAL 1 20
 FT CHAIN 21 119 BY SIMILARITY.
 FT DISULFID 45 100 BETA-2-MICROGLOBULIN.
 SQ SEQUENCE 119 AA; 13725 MW; 04A4DFE8FBC0CE CRC64;

Query Match 1.8%; Score 7; DB 1; Length 119;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LVLVLC 29
 |||||
 Db 9 LVLVLC 15

RESULT 15
 B2MG_CHISA STANDARD; PRT; 119 AA.
 ID B2MG_CHISA
 AC 077532;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Beta-2-microglobulin precursor.
 GN B2M.
 OS Chiropotes satanas (Black-bearded saki).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Pitheciinae;
 OC Chiropotes.
 OX NCBI_TaxID=9525;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=98298008; PubMed=9634477;
 RA Canavez F.C., Ladasky J.J., Muniz J.A.P.C., Seunarez H.N., Parham P.;
 RT "Beta-2-microglobulin in neotropical primates (Platyrrhini).";
 RL Immunogenetics 48:133-140(1998).
 CC -!- FUNCTION: BETA-2-MICROGLOBULIN IS THE BETA-CHAIN OF MAJOR
 CC HISTOCOMPATIBILITY COMPLEX CLASS I MOLECULES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC
 DR EMBL; AF032075; AAC52097.1; -;
 DR EMBL; AF032074; AAC52097.1; JOINED.
 DR HSSP; P01884; 1A6Z.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_C1.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00407; IgC1; 1.
 DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
 DR MHC I; Signal; 1.
 FT SIGNAL 1 20
 FT CHAIN 21 119 BY SIMILARITY.
 FT DISULFID 45 100 BETA-2-MICROGLOBULIN.
 SQ SEQUENCE 119 AA; 13657 MW; BCB35491EFD6F3E CRC64;

Query Match 1.8%; Score 7; DB 1; Length 119;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LVLVLC 29
 |||||
 Db 9 LVLVLC 15

Search completed: February 12, 2003, 11:10:47
 Job time : 16 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:08:01 ; Search time 38 Seconds
(without alignments)
1336.013 Million cell updates/sec

Title: US-09-623-035-2

Perfect score: 381

Sequence: 1 MTVARPSVPAALPLGLGLPR.....HTCFLLTGLGLTWGLLT 381

Scoring table: OLIGO #
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

A.Geneseq_101002:*

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
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20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	381	100.0	381	8 AAP70048	Human decay accele
2	381	100.0	381	16 AAP74773	Decay accelerating
3	381	100.0	381	16 AAR66683	Decay accelerating
4	381	100.0	381	20 AAY31740	Human CD55 and 791
5	381	100.0	381	20 AAW73505	Decay accelerating
6	361	94.8	440	8 AAP70049	Human decay accele
7	361	94.8	440	10 AAP94774	Membrane bound dec
8	361	94.8	440	16 AAR66684	Decay accelerating
9	361	94.8	440	18 AAW27483	Human glycophospha
10	323	84.8	577	17 AAW06882	Membrane co-factor

11	323	84.8	611	22 AAE12569	CAR2 protein. Uni
12	323	84.8	611	22 AAE03762	CAR-2 chimeric pro
13	323	84.8	611	22 AAE16794	CAR2 protein. Uni
14	299	78.5	299	17 AAW06881	Decay accelerating
15	296	77.7	376	20 AAY50035	Human complement r
16	296	77.7	381	18 AAW26317	Human decay accele
17	286	75.1	320	22 AAG68150	Codon modified hum
18	280	73.5	458	22 AAG75594	Human colon cancer
19	251	65.9	254	23 ABB07541	Amino acid sequenc
20	251	65.9	271	23 ABB07542	Amino acid sequenc
21	93	24.4	367	15 AAR50087	MCP:DAF fusion pro
22	65	17.1	182	21 AAB53601	Human colon cancer
23	37	9.7	37	21 AAY49760	Compact structure
24	37	9.7	37	21 AAY88076	DAF GPI anchor pep
25	37	9.7	37	21 AAY43820	Membrane anchoring
26	37	9.7	37	22 ABA45935	Transdominant effe
27	37	9.7	37	22 AAB35067	DAF membrane ancho
28	37	9.7	37	23 ABB07746	Membrane-anchoring
29	37	9.7	37	23 AAU76173	Decay accelerating
30	37	9.7	42	18 AAW19903	Fusion of FcRn hea
31	37	9.7	42	18 AAW19906	Fusion of beta 2-m
32	37	9.7	248	18 AAN37341	DR alpha-DAF chime
33	37	9.7	261	18 AAN37342	DR beta-1-DAF chim
34	37	9.7	272	17 AAR92254	Neutral cell adhesi
35	29	7.6	29	15 AAR50086	Decay accelerating
36	23	6.0	41	20 AAY04334	Fragment of human
37	20	5.2	117	20 AAW86134	Protein sequence o
38	19	5.0	37	13 AAR20964	Sequence of decay
39	16	4.2	1006	21 AAY44455	Modified T. cruzi
40	10	2.6	10	22 AAG96997	Human complementar
41	10	2.6	10	22 AAG96999	Human complementar
42	10	2.6	10	22 AAG97001	Human complementar
43	10	2.6	10	22 AAG97003	Human complementar
44	10	2.6	10	22 AAG97005	Human complementar
45	10	2.6	10	22 AAG97007	Human complementar

ALIGNMENTS

RESULT 1	
AAAP70048	
ID	AAAP70048 standard; protein; 381 AA.
XX	
AC	AAAP70048:
XX	
DT	03-OCT-2002 (updated)
DT	03-FEB-1991 (first entry)
DE	Human decay acceleration factor variant #1.
XX	
KW	Decay acceleration factor.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Region
FT	Location/Qualifiers
XX	331..347
XX	/label-putative transmembrane region
PN	EP244267-A.
XX	
PD	04-NOV-1987.
XX	
PF	01-MAY-1987; 87EP-0303944.
XX	
PR	02-MAY-1986; 86US-0859107.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Carras IW;
XX	
DR	WPI; 1987-308481/44.
DR	N-PSDB; AAN70047.

XX New decay accelerating factor variants - obtained with the factor by
 PT using recombinant DNA procedures.
 XX
 XX
 PS Disclosure; Page 15-17; 20pp; English.
 XX
 CC The probable phosphatidylinositol derivatization site is Cys(330).
 CC The DAF variant is useful for treating paroxysmal nocturnal
 CC haemoglobinuria, or inflammatory or cell lytic autoimmune
 CC diseases. It may be used to ameliorate allograft rejection
 CC or autoimmune diseases. See also AAN70046, AAN70048.
 CC (Updated on 03-OCT-2002 to add missing OS field.)
 CC
 XX
 SQ Sequence 381 AA:

Query Match 100.0%; Score 381; DB 8; Length 381;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYVARSVAALPLGELPRLLLVLLCPAYWGDCGLPPDVNAPALGRTSPEDTV 60
 DB 1 MYVARSVAALPLGELPRLLLVLLCPAYWGDCGLPPDVNAPALGRTSPEDTV 60
 QY 61 IYKCEESFVKIPGKDSVYICLKGSQMSDIEFCNRSCEVPRRLNSASIKOPYITQNYPP 120
 DB 61 IYKCEESFVKIPGKDSVYICLKGSQMSDIEFCNRSCEVPRRLNSASIKOPYITQNYPP 120
 QY 121 VGTVEYECRPGYRRPSPKLTCLQNLKMSAVFECKKSCPNNGEIRNGIDVPGGI 180
 DB 121 VGTVEYECRPGYRRPSPKLTCLQNLKMSAVFECKKSCPNNGEIRNGIDVPGGI 180
 QY 181 LGATISFCNNGYKLFGSTSFCLISGSSVQMSDLPFCRELYCAPAQIDNGIIQGER 240
 DB 181 LGATISFCNNGYKLFGSTSFCLISGSSVQMSDLPFCRELYCAPAQIDNGIIQGER 240
 QY 241 DHYGYROSTYACNKGFTMIGESHYCTVNNDEGEMSGPPRECGRKSLTSKVPYQKPT 300
 DB 241 DHYGYROSTYACNKGFTMIGESHYCTVNNDEGEMSGPPRECGRKSLTSKVPYQKPT 300
 QY 301 TVNVPTEVSPTSOKTTTTPPNAQATSTPVSRTKHFHETTPKKGSGTSGTTRLLS 360
 DB 301 TVNVPTEVSPTSOKTTTTPPNAQATSTPVSRTKHFHETTPKKGSGTSGTTRLLS 360
 QY 361 GHTCFTLGLGLGVYTMGLLT 381
 DB 361 GHTCFTLGLGLGVYTMGLLT 381

RESULT 2
 AAP94773
 ID AAP94773 standard; protein; 381 AA.
 XX
 AC AAP94773;
 XX
 DT 04-JUL-1990 (first entry)
 XX
 DE Decay accelerating factor (DAF) of clones lambda 33 and lambda 47.
 XX
 KW DAF; allograft rejection; affinity purification;
 KW autoimmune disease; ds.
 XX
 OS Synthetic.
 XX
 PN W08901041-A.
 XX
 PD 09-FEB-1989.
 XX
 PF 03-AUG-1988; 88WO-US02648.
 XX
 PR 06-AUG-1987; 87US-0083757.
 XX
 PA (GETH) GENETECH INC.
 XX

PI Caras I;
 XX
 XX WPI; 1989-061177/08.
 DR N-PSDB; AAN91043.
 XX
 PT Fusion polypeptide for targeting protein to cell membrane -
 PT comprises phospholipid anchor domain with heterologous
 PT polypeptide.
 XX
 PS Disclosure; 61pp; English.
 XX
 CC Recombinant DAF's are useful in treatment of inflammatory or cell lytic
 CC autoimmune diseases and allograft rejection. Useful in diagnostic
 CC compositions or in affinity purification.
 CC
 XX
 SQ Sequence 381 AA:

Query Match 100.0%; Score 381; DB 10; Length 381;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYVARSVAALPLGELPRLLLVLLCPAYWGDCGLPPDVNAPALGRTSPEDTV 60
 DB 1 MYVARSVAALPLGELPRLLLVLLCPAYWGDCGLPPDVNAPALGRTSPEDTV 60
 QY 61 IYKCEESFVKIPGKDSVYICLKGSQMSDIEFCNRSCEVPRRLNSASIKOPYITQNYPP 120
 DB 61 IYKCEESFVKIPGKDSVYICLKGSQMSDIEFCNRSCEVPRRLNSASIKOPYITQNYPP 120
 QY 121 VGTVEYECRPGYRRPSPKLTCLQNLKMSAVFECKKSCPNNGEIRNGIDVPGGI 180
 DB 121 VGTVEYECRPGYRRPSPKLTCLQNLKMSAVFECKKSCPNNGEIRNGIDVPGGI 180
 QY 181 LGATISFCNNGYKLFGSTSFCLISGSSVQMSDLPFCRELYCAPAQIDNGIIQGER 240
 DB 181 LGATISFCNNGYKLFGSTSFCLISGSSVQMSDLPFCRELYCAPAQIDNGIIQGER 240
 QY 241 DHYGYROSTYACNKGFTMIGESHYCTVNNDEGEMSGPPRECGRKSLTSKVPYQKPT 300
 DB 241 DHYGYROSTYACNKGFTMIGESHYCTVNNDEGEMSGPPRECGRKSLTSKVPYQKPT 300
 QY 301 TVNVPTEVSPTSOKTTTTPPNAQATSTPVSRTKHFHETTPKKGSGTSGTTRLLS 360
 DB 301 TVNVPTEVSPTSOKTTTTPPNAQATSTPVSRTKHFHETTPKKGSGTSGTTRLLS 360
 QY 361 GHTCFTLGLGLGVYTMGLLT 381
 DB 361 GHTCFTLGLGLGVYTMGLLT 381

RESULT 3
 AAR66683
 ID AAR66683 standard; protein; 381 AA.
 XX
 AC AAR66683;
 XX
 DT 23-JUL-1995 (first entry)
 XX
 DE Decay accelerating factor.
 XX
 KW Decay accelerating factor; DAF; mDAF; fusion protein; liposome;
 KW cell targeting; glycosphosphatidylinositol; GPI; drug delivery.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Peptide 1..34
 FT /Label= Sig_peptide
 FT Modified-site 364
 FT /note= "probable phosphatidylinositol
 XX derivatization site"
 XX
 PN US374548-A.

XX 20-DEC-1994.
 XX
 XX
 XX 02-MAY-1986; 86DS-0859107.
 XX
 XX
 XX 02-MAY-1986; 86DS-0859107.
 PR 06-AUG-1987; 87US-0083757.
 PR 19-DEC-1991; 91US-0811048.
 PR 12-FEB-1993; 93US-0017934.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Caras IW;
 XX
 XX WPI; 1995-035649/05.
 DR N-PSDB; AAQ79863.
 XX
 PT Liposome(s) for targeting particulate cells contg. fusion protein
 PT - of glyco:phosphatidyl:inositol anchor and heterologous
 PT targeting protein, e.g. for delivering toxins to infected or
 PT cancer cells.
 XX
 PS Disclosure; Fig. 1a-1f; 36pp; English.
 XX
 CC A probe (given in AAQ79863) based on the N-terminal sequence of human
 CC decay accelerating factor (DAF) was used to screen a HeLa cell
 CC lambda cDNA library. Isolated clones encoding membrane-bound DAF
 CC (MDAF) were obtained, and the full sequence of mDAF cDNA was
 CC determined (AAQ79863). The GPI signal domain of mDAF may be fused to
 CC a heterologous protein and targeted to cell membrane surfaces.
 XX
 SQ Sequence 381 AA;

Query Match 100.0%; Score 381; DB 16; Length 381;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVARSPVPAALPLGLGELPRLLLVLLCLPAVWGDCGLPPDVNPAQALGRTSFPEDTV 60
 DB 1 MTVARSPVPAALPLGLGELPRLLLVLLCLPAVWGDCGLPPDVNPAQALGRTSFPEDTV 60
 QY 61 IYKCESEFVKIPGEKDSVCLKGSQMSDIEFCNRSCEVPTRLNSALSKOPYTTONYFP 120
 DB 61 IYKCESEFVKIPGEKDSVCLKGSQMSDIEFCNRSCEVPTRLNSALSKOPYTTONYFP 120
 QY 121 VGTVEVECRPGYRREPSLSPKLTCLQNLKWSAVEFCRKKSCPNPEIRNGOIDVPGGI 180
 DB 121 VGTVEVECRPGYRREPSLSPKLTCLQNLKWSAVEFCRKKSCPNPEIRNGOIDVPGGI 180
 QY 181 LFGATISFSCNTGYKLGSTSFCLISGSSVQMSDPLPECREIYCPAPQIDNGIIGER 240
 DB 181 LFGATISFSCNTGYKLGSTSFCLISGSSVQMSDPLPECREIYCPAPQIDNGIIGER 240
 QY 241 DHGYSRVYACNKGFTMGESHSIYCTVNNDSGMSGPPPECRGKSLJTSKVPYVOKPT 300
 DB 241 DHGYSRVYACNKGFTMGESHSIYCTVNNDSGMSGPPPECRGKSLJTSKVPYVOKPT 300
 QY 301 TVNVPTEVPSISOKTITTTTTPNAQTRSTPVSRITKHHETTPNKGSGTGTLLS 360
 DB 301 TVNVPTEVPSISOKTITTTTTPNAQTRSTPVSRITKHHETTPNKGSGTGTLLS 360
 QY 361 GHRCFTLTGLGLTVMGLLT 381
 DB 361 GHRCFTLTGLGLTVMGLLT 381

RESULT 4
 AA31740
 ID AA31740 standard; Protein; 381 AA.
 XX
 AC AA31740;
 XX
 DT 22-NOV-1999 (first entry)

Applicant's
 own
 in 10

XX Human CD55 and 791tgp72 tumour associated antigen.
 DE
 XX
 KW CD55; decay accelerating factor; DAF; tumour associated antigen;
 KW 791tgp72; colorectal cancer; breast cancer; ovary cancer;
 KW osteosarcoma; vaccine; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..34
 FT Protein /note="signal peptide"
 FT 35..380
 XX /note="mature protein"
 PN WO943800-A1.
 XX
 XX 02-SEP-1999.
 XX
 XX 26-FEB-1999; 99MO-GB00582.
 XX
 XX 26-FEB-1998; 98GB-0004065.
 XX
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 PI Durrant IG, Spendlove I;
 XX
 DR WPI; 1999-540585/45.
 DR N-PSDB; AA87914, AA87915.
 XX
 PT Cancer vaccine containing CD55 family polypeptide, to induce at
 PT least one of T helper, cytotoxic T cell or natural killer immune
 PT response
 XX
 PS Claim 4; Fig 10; p 82pp; English.
 XX
 CC The present sequence represents a new human tumour associated
 CC antigen, 791tgp72, which is over-expressed on a wide range of solid
 CC tumours. The amino acid sequence of 791tgp72 is identical to that
 CC of human CD55, although the glycosylation patterns of the 2
 CC proteins are different. CD55 and 791tgp72 are encoded by cDNAs
 CC (see AA87914 and AA87915) which are identical over the entire coding
 CC region, but differ in the 5' and 3' non-coding regions. A claimed
 CC cancer vaccine comprises a polypeptide of the CD55 family, including
 CC full-length CD55 or 791tgp72, or an antigen, polypeptide, fragment
 CC or derivative of CD55 or 791tgp72. Claimed cancer vaccines also
 CC include nucleic acids encoding CD55 or 791tgp72 antigen,
 CC polypeptide, fragment or derivative. Claimed methods of treating a
 CC cancer patient involve administering the claimed vaccine. A method
 CC of isolating 791tgp72 antigen from cells expressing the antigen
 CC is also claimed. The cancer vaccines induce at least one of T
 CC helper, cytotoxic T cell or natural killer immune responses,
 CC possibly also production of neutralizing antibodies and complement-
 CC mediated lysis. They are useful for treating e.g. colorectal,
 CC breast or ovarian cancer or osteosarcoma, where these are
 CC associated with overexpression of 791tgp72.
 XX
 SQ Sequence 381 AA;

Query Match 100.0%; Score 381; DB 20; Length 381;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVARSPVPAALPLGLGELPRLLLVLLCLPAVWGDCGLPPDVNPAQALGRTSFPEDTV 60
 DB 1 MTVARSPVPAALPLGLGELPRLLLVLLCLPAVWGDCGLPPDVNPAQALGRTSFPEDTV 60
 QY 61 IYKCESEFVKIPGEKDSVCLKGSQMSDIEFCNRSCEVPTRLNSALSKOPYTTONYFP 120
 DB 61 IYKCESEFVKIPGEKDSVCLKGSQMSDIEFCNRSCEVPTRLNSALSKOPYTTONYFP 120
 QY 121 VGTVEVECRPGYRREPSLSPKLTCLQNLKWSAVEFCRKKSCPNPEIRNGOIDVPGGI 180
 DB 121 VGTVEVECRPGYRREPSLSPKLTCLQNLKWSAVEFCRKKSCPNPEIRNGOIDVPGGI 180

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Db 121 VGVVVEECRPGYRRRPSLSPKLTCLQNLKWSVAVEFCKKKSCPNPGEIRNGQIDVPGGI 180
QY 181 LGGATISFCSCNTGYKLFSGTSSFCCLISGSSVQMSDPLPECREIYCPAPQIDNGIIQGER 240
Db 181 LGGATISFCSCNTGYKLFSGTSSFCCLISGSSVQMSDPLPECREIYCPAPQIDNGIIQGER 240
QY 241 DHYGYROSATYACNKGFTMIGESHIYCTVNNDEGEMSGPPRECCKSLTSKVPPTYOKPT 300
Db 241 DHYGYROSATYACNKGFTMIGESHIYCTVNNDEGEMSGPPRECCKSLTSKVPPTYOKPT 300
QY 301 TVNVPTEVSPTSOKTTTTPNQAOTRSTPVSRTTKHFHETTPNKGSGTSGTTRLLS 360
Db 301 TVNVPTEVSPTSOKTTTTPNQAOTRSTPVSRTTKHFHETTPNKGSGTSGTTRLLS 360
QY 361 GHTCFTLTGLTGLTYMGLLT 381
Db 361 GHTCFTLTGLTGLTYMGLLT 381

RESULT 5
AAW73505
ID AAW73505 standard; Protein; 381 AA.
AC AAW73505;
DT 01-MAR-1999 (first entry)
XX
DE Decay accelerating factor protein.
XX
KM DAF; decay accelerating factor; human; compliment protein; gene therapy;
XX viral vector; ds.
XX
OS Homo sapiens.
XX
PN JP10313865-A.
XX
PD 02-DEC-1998.
XX
PF 15-MAY-1997; 97JP-0125965.
XX
PR 15-MAY-1997; 97JP-0125965.
XX
PA (DINA-) DINABEKU KENKYUSHO KK.
XX
DR WPT; 1999-074147/07.
XX
DR N-PSDB; AAW08935.
XX
PT Vector having complement controlling factor - useful for gene
PT therapy
XX
PS Example 3; Page 8-9; 15pp; Japanese.
XX
CC This sequence is the human decay accelerating factor (DAF) protein.
CC DAF can be used in the viral vector of the invention. The viral vector
CC contains a factor controlling the function of a human complement protein,
CC particularly a membrane combining type protein. The viral vector, which
CC is stable in situ, is useful for gene therapy.
XX
SQ Sequence 381 AA;

Query Match 100.0%; Score 381; DB 20; Length 381;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVARSPVAALPLLGELPRLLLVLLCLPAVWGCGLPDPVNPAPALEGRTSPEDTY 60
Db 1 MTVARSPVAALPLLGELPRLLLVLLCLPAVWGCGLPDPVNPAPALEGRTSPEDTY 60
QY 61 IITYKEESFVKIPGKDSYICLKGSQMSDIEFCNRSCEVPTRLNSASLQPYITQNTFP 120
Db 61 IITYKEESFVKIPGKDSYICLKGSQMSDIEFCNRSCEVPTRLNSASLQPYITQNTFP 120
QY 121 VGVVVEECRPGYRRRPSLSPKLTCLQNLKWSVAVEFCKKKSCPNPGEIRNGQIDVPGGI 180

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Db 121 VGVVVEECRPGYRRRPSLSPKLTCLQNLKWSVAVEFCKKKSCPNPGEIRNGQIDVPGGI 180
QY 181 LGGATISFCSCNTGYKLFSGTSSFCCLISGSSVQMSDPLPECREIYCPAPQIDNGIIQGER 240
Db 181 LGGATISFCSCNTGYKLFSGTSSFCCLISGSSVQMSDPLPECREIYCPAPQIDNGIIQGER 240
QY 241 DHYGYROSATYACNKGFTMIGESHIYCTVNNDEGEMSGPPRECCKSLTSKVPPTYOKPT 300
Db 241 DHYGYROSATYACNKGFTMIGESHIYCTVNNDEGEMSGPPRECCKSLTSKVPPTYOKPT 300
QY 301 TVNVPTEVSPTSOKTTTTPNQAOTRSTPVSRTTKHFHETTPNKGSGTSGTTRLLS 360
Db 301 TVNVPTEVSPTSOKTTTTPNQAOTRSTPVSRTTKHFHETTPNKGSGTSGTTRLLS 360
QY 361 GHTCFTLTGLTGLTYMGLLT 381
Db 361 GHTCFTLTGLTGLTYMGLLT 381

RESULT 6
AAP70049
ID AAP70049 standard; protein; 440 AA.
AC AAP70049;
DT 03-FEB-1991 (first entry)
XX
DE Human decay acceleration factor variant #2.
XX
KM Decay acceleration factor; SDAF.
XX
OS Homo sapiens.
XX
PN EP244267-A.
XX
PD 04-NOV-1987.
XX
PF 01-MAY-1987; 87EP-0303944.
XX
PR 02-MAY-1986; 86US-0859107.
XX
PA (GETH ) GENENTECH INC.
XX
PT Caras IW;
XX
DR WPT; 1987-308481/44.
XX
DR N-PSDB; AAN70048.
XX
PT New decay accelerating factor variants - obtained with the factor by
PT using recombinant DNA procedures.
XX
PS Disclosure; Page 18-20; 20pp; English.
XX
CC The protein sequence is a variant of decay acceleration factor, SDAF.
CC DAF and variants are useful for treating paroxysmal nocturnal
CC haemoglobinuria, or inflammatory or cell lytic autoimmune diseases.
CC They may be used to ameliorate allograft rejection or autoimmune
CC diseases.
XX
SQ See also AAN70046 and AAN70047.

Query Match 94.8%; Score 361; DB 8; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVARSPVAALPLLGELPRLLLVLLCLPAVWGCGLPDPVNPAPALEGRTSPEDTY 60

```


CC A probe (given in AA079865) based on the N-terminal sequence of human
CC decay accelerating factor (DAF) was used to screen a HeLa cell
CC lambda cDNA library. Isolated clones encoding soluble DAF
CC (sDAF) were obtained; the full sequence of sDAF cDNA is given in
CC AA079864 and the deduced protein sequence in AA06684.
XX

Sequence 440 AA:

Query Match 94.8%; Score 361; DB 16; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVARPSVPAALPLIGELRLILVLCIPAYWGDCGLPPDVNAPALEGRTSPEDTV 60
DB 1 MTVARPSVPAALPLIGELRLILVLCIPAYWGDCGLPPDVNAPALEGRTSPEDTV 60
QY 61 IYKCESEFVKIPGEKDSVYICKGSQMSDIEFCNRSCEVPTRLNSASLKOPYITONFPP 120
DB 61 IYKCESEFVKIPGEKDSVYICKGSQMSDIEFCNRSCEVPTRLNSASLKOPYITONFPP 120
QY 121 VGTVEYECRPGYRRPSPISPKITCLONLKMWSTAVEFCKKSCPNPGEIRNGQIDVPGGI 180
DB 121 VGTVEYECRPGYRRPSPISPKITCLONLKMWSTAVEFCKKSCPNPGEIRNGQIDVPGGI 180
QY 181 LFGATISFSCNTGYKLFGSTSFCLISGSSVQMSDPLPCREITYCPAPQIDNGITIOGER 240
DB 181 LFGATISFSCNTGYKLFGSTSFCLISGSSVQMSDPLPCREITYCPAPQIDNGITIOGER 240
QY 241 DHYGRQSVTVACNKGFTMIGHSIYCTVNNDEGEMSGPPRCRGSLSKVPPTVOKPT 300
DB 241 DHYGRQSVTVACNKGFTMIGHSIYCTVNNDEGEMSGPPRCRGSLSKVPPTVOKPT 300
QY 301 TVNVPTTEVSPTISQKTTTTPPNAQATRSPTVSKTKHFHETTPNKGSGTSGTTRLLS 360
DB 301 TVNVPTTEVSPTISQKTTTTPPNAQATRSPTVSKTKHFHETTPNKGSGTSGTTRLLS 360
QY 361 G 361
DB 361 G 361

RESULT 9
AAW27483
ID AAW27483 standard; Protein; 440 AA.
XX
AC AAW27483;

14-APR-1998 (first entry)

Human glycoposphatidylinositol anchored DAF.

Human; glycoposphatidylinositol; GPI; anchored DAF; surface;
homologous complement restriction factor; HCRF; medical apparatus;
medical dressing; surgical equipment; diagnostic kit; prevention;
purification device; reduction; complement activation.

Homo sapiens.

Key Location/Qualifiers
FT Peptide 1..34
FT Peptide /label= sig_peptide
FT Peptide 35..440
FT Peptide /label= mat_peptide

W09735886-A1.

02-OCT-1997.

12-MAR-1997; 97WO-GB00684.

31-OCT-1996; 96GB-0022694.

22-MAR-1996; 96GB-0006073.

28-MAR-1996; 96GB-0006516.

XX (IMOT-) IMOTRAN LTD.
PA
XX
XX Watkins NJ;
PI
XX
XX
DR MPI: 1997-489571/45.
DR N-PSDB: AAT90287.
XX

Surfaces which prevent or reduce complement activation - having
surface bound homologous complement restriction factor
Example 1; Fig 1; 50pp; English.

The present sequence is human glycoposphatidylinositol (GPI)
anchored DAF. GPI anchored DAF was used in the development of a
novel surface bound to a homologous complement restriction factor
(HCRF), where the surface is not a surface to which HCRF binds in
vivo. The surface can be used in medical apparatus (e.g.
extra-corporeal circulation systems, tubing, valves, membranes,
pumps, oxygenators, catheters, cannulas, fluid reservoirs or
prostheses), medical dressings, surgical equipment, diagnostic kits
(e.g. kits for determining whether a patient has an abnormality
which prevents the complement system from working normally or from
being properly regulated) and purification devices (e.g. for
purifying complement components). The surface can be used to reduce
or prevent activation of complement, and to reduce morbidity due to
complement activation.

Sequence 440 AA:

Query Match 94.8%; Score 361; DB 18; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVARPSVPAALPLIGELRLILVLCIPAYWGDCGLPPDVNAPALEGRTSPEDTV 60
DB 1 MTVARPSVPAALPLIGELRLILVLCIPAYWGDCGLPPDVNAPALEGRTSPEDTV 60
QY 61 IYKCESEFVKIPGEKDSVYICKGSQMSDIEFCNRSCEVPTRLNSASLKOPYITONFPP 120
DB 61 IYKCESEFVKIPGEKDSVYICKGSQMSDIEFCNRSCEVPTRLNSASLKOPYITONFPP 120
QY 121 VGTVEYECRPGYRRPSPISPKITCLONLKMWSTAVEFCKKSCPNPGEIRNGQIDVPGGI 180
DB 121 VGTVEYECRPGYRRPSPISPKITCLONLKMWSTAVEFCKKSCPNPGEIRNGQIDVPGGI 180
QY 181 LFGATISFSCNTGYKLFGSTSFCLISGSSVQMSDPLPCREITYCPAPQIDNGITIOGER 240
DB 181 LFGATISFSCNTGYKLFGSTSFCLISGSSVQMSDPLPCREITYCPAPQIDNGITIOGER 240
QY 241 DHYGRQSVTVACNKGFTMIGHSIYCTVNNDEGEMSGPPRCRGSLSKVPPTVOKPT 300
DB 241 DHYGRQSVTVACNKGFTMIGHSIYCTVNNDEGEMSGPPRCRGSLSKVPPTVOKPT 300
QY 301 TVNVPTTEVSPTISQKTTTTPPNAQATRSPTVSKTKHFHETTPNKGSGTSGTTRLLS 360
DB 301 TVNVPTTEVSPTISQKTTTTPPNAQATRSPTVSKTKHFHETTPNKGSGTSGTTRLLS 360
QY 361 G 361
DB 361 G 361

RESULT 10
AAW06882
ID AAW06882 standard; Protein; 577 AA.
XX
AC AAW06882;

18-MAR-1997 (first entry)

Membrane co-factor protein-decay accelerating factor hybrid.

KM Complement inhibitor; membrane co-factor protein; MCP;
 KM decay accelerating factor; DAF; chimeric protein; glycosaminoglycan;
 KM heparin; cell lysis; sepsis; adult respiratory distress syndrome;
 KM reperfusion injury; cell damage.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..254
 FT /label= MCP
 FT 255..577
 FT Region /label= DAF
 XX
 PN WO634965-A2.
 XX
 PD 07-NOV-1996.
 XX
 PF 03-MAY-1996; 96WO-US06301.
 XX
 PR 05-MAY-1995; 95US-0435149.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Creasey AA, Innis MA, Zaror I;
 DR WPI: 1996-506167/50.
 DR N-PSDB; AAT46065.
 XX
 PT Chimeric proteins for inhibiting complement-mediated cell lysis -
 PT comprise membrane co-factor protein and decay accelerating factor
 PT peptide sequences
 XX
 PS Disclosure; Page 25-26; 33pp; English.
 XX
 CC A hybrid protein (AAM06882) comprises portions (see also AAM06880-81)
 CC of the complement-inhibitors membrane co-factor protein (MCP) and
 CC decay accelerating factor (DAF). It can be used in novel chimeric
 CC proteins also incorporating a peptide (AAM06875-79, AAM06883-90) able
 CC to bind glycosaminoglycans (esp. heparin) present on cell surfaces.
 CC The constructs are encoded by overlapping PCR (see also AAT46066-72)
 CC using MCP-DAF hybrid DNA (AAT46065) as template, and can be expressed
 CC in e.g. insect cells. The chimeric proteins are directed to cell
 CC surfaces where they inhibit complement-mediated cell lysis. They
 CC are used to treat and prevent disease states in which complement
 CC plays a role, e.g. sepsis, adult respiratory distress syndrome,
 CC reperfusion injury and tissue damage.
 CC
 XX
 SQ Sequence 577 AA:
 Query Match 84.8%; Score 323; DB 17; Length 577;
 Best Local Similarity 100.0%; Pred. No. 5.4e-298;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 35 DCGLPVPVNAQPALERTSPEDVTITTCESFVKIPGKDSVTLKKSQMSDIEFC 94
 DB 255 DCGLPVPVNAQPALERTSPEDVTITTCESFVKIPGKDSVTLKKSQMSDIEFC 314
 QY 95 NRSCVEVTRNLNSLAKOPYITTONTFPGIVGEVCECRPGYRREPSLSKRLCLQNLKWSA 154
 DB 315 NRSCVEVTRNLNSLAKOPYITTONTFPGIVGEVCECRPGYRREPSLSKRLCLQNLKWSA 374
 QY 155 VERCKKSCNPGEIRNGQIDVPGILFGATISFCNTGYKLFQSTSSFCLLISGSSVQWS 214
 DB 375 VERCKKSCNPGEIRNGQIDVPGILFGATISFCNTGYKLFQSTSSFCLLISGSSVQWS 434
 QY 215 DPLPECEITICPAPQIDNGLIGERDHYGRQSVYTAACKGFTMIEHSITCYVNDDEG 274
 DB 435 DPLPECEITICPAPQIDNGLIGERDHYGRQSVYTAACKGFTMIEHSITCYVNDDEG 494
 QY 275 EMSGPPPECKGSLTSKVPPTVOKPTTVNVPTFEVSPTSOKTKTKTTTPNAQATRSPTVS 334
 DB 495 EMSGPPPECKGSLTSKVPPTVOKPTTVNVPTFEVSPTSOKTKTKTTTPNAQATRSPTVS 554

QY 335 RTTKHFHETTPNKGSGTTSCTTR 357
 DB 555 RTTKHFHETTPNKGSGTTSCTTR 577
 RESULT 11
 ID AAE12569
 XX AAE12569 standard; Protein; 611 AA.
 AC AAE12569;
 XX
 DT 03-JAN-2002 (first entry)
 XX
 DE CAB2 protein.
 XX
 KM Expression vector: crippled selectable marker; neomycin resistance;
 KM HIV protein; human immunodeficiency virus; improved expression; CAB2;
 KM CAB4; amplifiable selectable marker; dihydrofolate reductase; dhfr;
 KM transgene; continuous cell line preparation.
 XX
 OS Unidentified.
 XX
 PN US2001024807-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 22-DEC-2000; 2000US-0748061.
 XX
 PR 01-NOV-1999; 99US-162930P.
 PR 30-DEC-1999; 99US-0475460.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Innis M, Scott EM;
 DR WPI: 2001-638503/73.
 DR N-PSDB; AAD20355.
 XX
 PT New expression vector, useful for improving expression of transgene or
 PT polypeptide, comprises 3 polynucleotides encoding crippled selectable
 PT marker, heterologous polypeptide or second amplifiable selectable
 PT marker -
 XX
 PS Example 2; Fig 1; 27pp; English.
 CC The invention relates to a new expression vector comprising a first
 CC polynucleotide encoding a first, crippled selectable marker which
 CC include sequences encoding antibiotic (neomycin) resistance containing
 CC one or more crippling mutations; second polynucleotide encoding a
 CC heterologous polypeptide of interest which is viral protein (e.g., an
 CC HIV protein) or is CAB2 or CAB4; and a third polynucleotide encoding
 CC a second amplifiable selectable marker e.g. dihydrofolate reductase
 CC (dhfr). The expression vectors are useful for the efficient expression
 CC of desired polypeptides or improving expression of a transgene of
 CC interest. The transformed cells can be used in the preparation of
 CC continuous cell lines in which the cells are essentially immortal or
 CC for the preparation of established cell lines that have the potential
 CC to be subcultured in vitro. The present sequence is CAB2 protein.
 CC Aberrant splicing of CAB2 DNA was corrected by removing donor and
 CC acceptor sites using overlapping PCR.
 XX
 SQ Sequence 611 AA:
 Query Match 84.8%; Score 323; DB 22; Length 611;
 Best Local Similarity 100.0%; Pred. No. 5.7e-298;
 Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 35 DCGLPVPVNAQPALERTSPEDVTITTCESFVKIPGKDSVTLKKSQMSDIEFC 94
 DB 289 DCGLPVPVNAQPALERTSPEDVTITTCESFVKIPGKDSVTLKKSQMSDIEFC 348
 QY 95 NRSCVEVTRNLNSLAKOPYITTONTFPGIVGEVCECRPGYRREPSLSKRLCLQNLKWSA 154

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Db 349 NNSCEVPTRLNSASLKQPYITONYPFVGTVVEYECRPGYRRRPSLSPKLTCLQNLKWSYA 408
Qy 155 VEFCKKSSCPNPGELRNGQIDVPGGILFGATISFSCNTGYKILFGSTSSFCILSGSSVQMS 214
Db 409 VEFCKKSSCPNPGELRNGQIDVPGGILFGATISFSCNTGYKILFGSTSSFCILSGSSVQMS 468
Qy 215 DPLPECREITCPAPPOIDNGIIOGERDHYGROSVTYACNKGFTMGEHSITCTVANNDEG 274
Db 469 DPLPECREITCPAPPOIDNGIIOGERDHYGROSVTYACNKGFTMGEHSITCTVANNDEG 528
Qy 275 EMSGPPPECRGKSLTSKVPPTVQKPTTVNVPPTTEVSPTSQKTTTTPNAQATSTPVS 334
Db 529 EMSGPPPECRGKSLTSKVPPTVQKPTTVNVPPTTEVSPTSQKTTTTPNAQATSTPVS 588
Qy 335 RTTKHFHETTPNKGSGTTSQTTR 357
Db 589 RTTKHFHETTPNKGSGTTSQTTR 611

RESULT 12
AAE03762 standard; Protein; 611 AA.
AC AAE03762;
XX 07-AUG-2001 (first entry)
DE CAB-2 chimeric protein.
XX Expression vector: crippled selectable marker; CAB-2; chimeric protein;
XX heterologous polypeptide; amplifiable selectable marker;
XX viral glycoprotein; membrane cofactor protein; MCP;
XX decay accelerating factor; DAF; complement activation.
XX Unidentified.
XX WO200132901-A1.
XX 10-MAY-2001.
XX 30-DEC-1999; 99WO-US31275.
XX 01-NOV-1999; 99US-0162980.
XX (CHIR ) CHIRON CORP.
XX Innis M, Scott E;
XX WPI: 2001-389720/41.
XX N-PSDB; AAD08170.
XX Expression vectors comprising a first, crippled selectable marker and a
XX second, amplifiable selectable marker for improved production of
XX polypeptides -
XX Example 1; Fig 1; 71pp; English.
XX The present invention relates to expression vector comprising a first
XX polynucleotide encoding a first, crippled selectable marker, a second
XX polynucleotide encoding a heterologous polypeptide of interest and a
XX third polynucleotide encoding a second, amplifiable selectable marker.
XX The vector is useful for producing a polypeptide such as CAB-2, CAB-4,
XX uPAR, VEGF-D and a viral protein, especially a viral glycoprotein. The
XX expression vector solve the problems of low yield and varied expression
XX levels by using a crippled first selectable marker linked to a transgene
XX and a second, amplifiable marker, which contains a disabling mutation.
XX The tedious process of identification of high expression loci in
XX mammalian cells is eliminated and provides an efficient mechanism by
XX which any desired polypeptide can be expressed at high levels using the
XX novel cell lines generated. In addition, altering the transgene such
XX that aberrant splicing is corrected may increase expression.
XX The present sequence is CAB-2 chimeric protein that
XX combines features of membrane cofactor protein (MCP) and decay

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CC accelerating factor (DAF) to inhibit complement activation.
CC The codons in the donor sites and acceptor sites of CAB-2 DNA are
CC changed for the correction of aberrant mRNA splicing.
SQ Sequence 611 AA:
Query Match 84.8%; Score 323; DB 22; Length 611;
Best Local Similarity 100.0%; Pred. No. 5,7e-298;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 35 DGLPDPVNAOPALEGRSPFEDYITTKCESFYKIPGENDSYCLKGSQMSDIEFC 94
Db 289 DGLPDPVNAOPALEGRSPFEDYITTKCESFYKIPGENDSYCLKGSQMSDIEFC 348
Qy 95 NNSCEVPTRLNSASLKQPYITONYPFVGTVVEYECRPGYRRRPSLSPKLTCLQNLKWSYA 154
Db 349 NNSCEVPTRLNSASLKQPYITONYPFVGTVVEYECRPGYRRRPSLSPKLTCLQNLKWSYA 408
Qy 155 VEFCKKSSCPNPGELRNGQIDVPGGILFGATISFSCNTGYKILFGSTSSFCILSGSSVQMS 214
Db 409 VEFCKKSSCPNPGELRNGQIDVPGGILFGATISFSCNTGYKILFGSTSSFCILSGSSVQMS 468
Qy 215 DPLPECREITCPAPPOIDNGIIOGERDHYGROSVTYACNKGFTMGEHSITCTVANNDEG 274
Db 469 DPLPECREITCPAPPOIDNGIIOGERDHYGROSVTYACNKGFTMGEHSITCTVANNDEG 528
Qy 275 EMSGPPPECRGKSLTSKVPPTVQKPTTVNVPPTTEVSPTSQKTTTTPNAQATSTPVS 334
Db 529 EMSGPPPECRGKSLTSKVPPTVQKPTTVNVPPTTEVSPTSQKTTTTPNAQATSTPVS 588
Qy 335 RTTKHFHETTPNKGSGTTSQTTR 357
Db 589 RTTKHFHETTPNKGSGTTSQTTR 611

RESULT 13
AAE16794 standard; Protein; 611 AA.
ID AAE16794
XX AAE16794;
XX 09-APR-2002 (first entry)
DE CAB2 protein.
XX Expression vector: crippled selectable marker; neomycin resistance;
XX HIV protein; human immunodeficiency virus; dihydrofolate reductase;
XX CAB2; CAB4; uronase-type plasminogen activator receptor; uPAR;
XX complement activation blocker; amplifiable selectable marker; dhfr;
XX vascular endothelial growth factor-D; VEGF-D.
XX Unidentified.
XX US6316253-B1.
XX 13-NOV-2001.
XX 30-DEC-1999; 99US-0475460.
XX 01-NOV-1999; 99US-162930P.
XX (CHIR ) CHIRON CORP.
XX Innis M, Scott EM;
XX WPI: 2002-121021/16.
XX N-PSDB; AAD27308.
XX An expression vector encoding a crippled neomycin resistance selectable
XX marker, a heterologous polypeptide and a amplifiable selectable marker,
XX useful for providing high expression of polypeptides in mammalian host
XX cells -

```

PS Example 2; Fig 1; 33pp: English.
XX
CC The invention relates to a new expression vector comprising a first
CC polynucleotide encoding a first, crippled selectable marker which
CC include sequences encoding antibiotic (neomycin) resistance containing
CC one or more crippling mutations; second polynucleotide encoding a
CC heterologous polypeptide of interest which is vital protein (e.g.
CC HIV protein) or is complement activation blocker (CAB)-2, CAB-4,
CC urokinase-type plasminogen activator receptor (uPAR) or vascular
CC endothelial growth factor-D (VEGF-D); and a third polynucleotide
CC encoding a second amplifiable selectable marker e.g. dihydrofolate
CC reductase (dhfr). The expression vector is used for stable, high
CC level expression of a polypeptide of interest in a host cell,
CC particularly mammalian cell or an insect cell. The present sequence
CC CAB2 protein. Aberrant splicing of CAB2 DNA was corrected by removing
CC donor and acceptor sites using overlapping PCR.
XX
SQ Sequence 611 AA;
Query Match 84.8%; Score 323; DB 23; Length 611;
Best Local Similarity 100.0%; Pred. No. 5.7e-298;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 DCGLPVPVNAQPALEGSTSPRETYITKCESEFVKIPGKDSYICLKGSQMSDIEEFC 94
DB 289 DCGLPVPVNAQPALEGSTSPRETYITKCESEFVKIPGKDSYICLKGSQMSDIEEFC 348
QY 95 NRSECVTRLNSASIKOPYITQNFEPYGVYECRPGYRREPSLSPKLTCLQNLKMSA 154
DB 349 NRSECVTRLNSASIKOPYITQNFEPYGVYECRPGYRREPSLSPKLTCLQNLKMSA 408
QY 155 VEFCKKSCPNPGRIRNGQIDVPGILFGATISFCNTGYLFGSTSSFCILSSSVQMS 214
DB 409 VEFCKKSCPNPGRIRNGQIDVPGILFGATISFCNTGYLFGSTSSFCILSSSVQMS 468
QY 215 DPLPECEHICYPAPQINDNGIIGERDHYGRQSYTAACNKGFTMIGHSIYCTVNNDEG 274
DB 469 DPLPECEHICYPAPQINDNGIIGERDHYGRQSYTAACNKGFTMIGHSIYCTVNNDEG 528
QY 275 EMSGPPPCRGKSLTSKVPYVOKPTVNVPTTEVSPTSOCTTKTTTPNAQATRSTPVS 334
DB 529 EMSGPPPCRGKSLTSKVPYVOKPTVNVPTTEVSPTSOCTTKTTTPNAQATRSTPVS 588
QY 335 RTTKHFHETTPNKGSGTSGTTR 357
DB 589 RTTKHFHETTPNKGSGTSGTTR 611
RESULT 14
AAW06881
ID AAW06881 standard; Protein: 299 AA.
XX
AC AAW06881;
XX
DT 18-MAR-1997 (first entry)
XX
DE Decay accelerating factor.
XX
KW Complement inhibitor; membrane co-factor protein; MCP;
KW decay accelerating factor; DAF; chimeric protein; glycosaminoglycan;
KW heparin; cell lysis; sepsis; adult respiratory distress syndrome;
KW reperfusion injury; cell damage.
XX
OS Homo sapiens.
XX
PN W09634965-A2.
XX
PD 07-NOV-1996.
XX
PF 03-MAY-1996; 96WO-US06301.
XX
PR 05-MAY-1995; 95US-0435149.
XX

PA (CHIR) CHIRON CORP.
XX
PI Creasey AA, Innis MA, Zaror I;
XX
DR WPI: 1996-506167/50.
XX
PT Chimeric proteins for inhibiting complement-mediated cell lysis
PT comprise membrane co-factor protein and decay accelerating factor
PT peptide sequences
XX
PS Disclosure; Page 25; 33pp: English.
XX
XX A portion (AAW06881) of the complement-inhibitor, decay accelerating
CC factor (DAF), is used in novel chimeric proteins of formula
CC A-R1-B-R2-C, where A and C are peptides (AAW06875-79, AAW06883-90) able
CC to bind glycosaminoglycans (esp. heparin) present on cell surfaces,
CC R1 is a portion of DAF or membrane co-factor protein (MCP, see also
CC AAW06880), R2 is DAF when R1 is MCP or MCP when R1 is DAF, and B is a
CC peptide that may have complement inhibitor activity. The chimeric
CC proteins (see also AAW06882) are directed to cell surfaces where they
CC inhibit complement-mediated cell lysis. They are used to treat and
CC prevent disease states in which complement plays a role, e.g.
CC sepsis, adult respiratory distress syndrome, reperfusion injury and
CC tissue damage.
XX
SQ Sequence 299 AA;
Query Match 78.5%; Score 299; DB 17; Length 299;
Best Local Similarity 100.0%; Pred. No. 1.8e-275;
Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 59 TVITKYCESEFVKIPGKDSYICLKGSQMSDIEEFCNRSCEVTRLNSASIKOPYITQNY 118
DB 1 TVITKYCESEFVKIPGKDSYICLKGSQMSDIEEFCNRSCEVTRLNSASIKOPYITQNY 60
QY 119 FPVGTVVEYECRPGYRREPSLSPKLTCLQNLKMSA VEFCKKSCPNPGEIRNGQIDVPG 178
DB 61 FPVGTVVEYECRPGYRREPSLSPKLTCLQNLKMSA VEFCKKSCPNPGEIRNGQIDVPG 120
QY 179 GILGATISFCNTGYLFGSTSSFCILSSSVQMSDPLPECRETYCPAPQINDNGIIG 238
DB 121 GILGATISFCNTGYLFGSTSSFCILSSSVQMSDPLPECRETYCPAPQINDNGIIG 180
QY 239 ERDHGYRQSYTAACNKGFTMIGHSIYCTVNNDEGEMSGPPPCRGKSLTSKVPYVOK 298
DB 181 ERDHGYRQSYTAACNKGFTMIGHSIYCTVNNDEGEMSGPPPCRGKSLTSKVPYVOK 240
QY 299 PTVNVPTTEVSPTSOCTTKTTTPNAQATRSTPVSRTTKHFHETTPNKGSGTSGTTR 357
DB 241 PTVNVPTTEVSPTSOCTTKTTTPNAQATRSTPVSRTTKHFHETTPNKGSGTSGTTR 299
RESULT 15
AAV50035
ID AAV50035 standard; Protein: 376 AA.
XX
AC AAV50035;
XX
DT 19-JAN-2000 (first entry)
XX
DE Human complement regulatory protein DAF.
XX
KW Complement regulatory protein; decay accelerating factor; DAF;
KW immune reaction; xenotransplantation; xenograft; transplant; organ;
KW rejection; hyperacute; inhibition; protection; heart; lung; liver;
KW kidney; pancreas; thyroid; islet cell; neurons; stem cell; tissue;
KW skin.
XX
OS Homo sapiens.
XX
PN W0953042-A2.
XX
PD 21-OCT-1999.
XX

```
XX 08-APR-1999; 99MO-GB01085.
PF
XX 09-APR-1998; 98GB-0007520.
PR
XX
XX (UYMA-) UNIV WALES COLLEGE OF MEDICINE.
PA
XX Morgan BP, Rushmore NK, Hinchliffe SJ, Van Den Berg CW;
PI
XX MPI; 1999-620420/53.
DR
XX
XX Use of cells or tissues expressing complement regulatory molecules for,
PT e.g. preventing xenotransplant rejection in humans
PT
XX
XX Claim 18; Fig 15; 88pp; English.
PS
XX
XX This sequence represents human complement regulatory protein DAF
CC (decay accelerating factor). Complement regulatory proteins (CRPs)
CC such as DAF and CD59 are membrane bound proteins that protect an
CC organism's cells from attack by its own complement. Hyperacute
CC rejection of a xenotransplant occurs because natural antibodies in
CC the human recipient bind to the endothelium of the donor organ and
CC activate complement, thereby initiating rapid rejection.
CC Hyperexpression of this protein in pig cells may be useful for the
CC protection of xenotransplanted organs, as greatly increased amounts
CC of functional CRP molecules will be expressed. The organ should be
CC resistant to attack by human complement, thus preventing organ
CC rejection. Methods of causing donor animal cells to hyperexpress CRPs
CC can be used for protection of xenotransplants. For example, organs,
CC tissue and cells can be generated which are resistant to complement
CC attack and hence to hyperacute rejection when transplanted into humans.
CC The methods can be used for organs, such as heart, lung, liver, kidney,
CC pancreas and thyroid; cells, such as islet cells, neurons, and stem
CC cells; or tissues, such as skin.
XX
SQ Sequence 376 AA:
Query Match 77.7%; Score 296; DB 20; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.6e-272;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 86 QMSDIEFCRSCSEVPTRLNSASLKOPIYQNTFVYGVYVEYECRPGYRREPSISPKLTC 145
DB 81 QMSDIEFCRSCSEVPTRLNSASLKOPIYQNTFVYGVYVEYECRPGYRREPSISPKLTC 140
OY 146 LQNLKMWSTAVEFCRCKKSCPNPGEIRNGQIDVPGGILFGATISFCNTGYKLFGSTSFCFL 205
DB 141 LQNLKMWSTAVEFCRCKKSCPNPGEIRNGQIDVPGGILFGATISFCNTGYKLFGSTSFCFL 200
OY 206 ISSSSVQMSDPLPECREIYCPAPQIDNGIIOGERDHYGRQSYTYACNKGFTMIGEHST 265
DB 201 ISSSSVQMSDPLPECREIYCPAPQIDNGIIOGERDHYGRQSYTYACNKGFTMIGEHST 260
OY 266 YCTVNNDEGMSGPPECRCKSLTSKYVPTVOKPTVNPTEVSPSTOKTTKTTTPNA 325
DB 261 YCTVNNDEGMSGPPECRCKSLTSKYVPTVOKPTVNPTEVSPSTOKTTKTTTPNA 320
OY 326 QATRSTPVASRTKHFHETTPNKGSGTTSCTRLLSGHTCFTLLGLGLTVMGLLT 381
DB 321 QATRSTPVASRTKHFHETTPNKGSGTTSCTRLLSGHTCFTLLGLGLTVMGLLT 376
```

Search completed: February 12, 2003, 11:10:26
Job time : 40 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:09:26 ; Search time 22 Seconds
(without alignments)
1664.873 Million cell updates/sec

Title: US-09-623-035-2
Perfect score: 381
Sequence: 1 MVARPSVPAALPLGLGELPR.....HTCFITLGLGLIVTMGLLT 381

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues
Word size : 0

Total number of hits satisfying chosen parameters: 283224
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR_73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	381	100.0	381	1 B26359	decay-accelerating
2	361	94.8	440	2 A26359	decay-accelerating
3	85	22.3	340	2 I56234	decay-accelerating
4	9	2.4	345	1 NBHU	apolipoprotein H p
5	9	2.4	2470	2 I50726	cation-independent
6	8	2.1	307	2 D83295	transaldolase PA27
7	8	2.1	347	2 G5283	asparaginase (EC 3
8	8	2.1	413	2 H75628	hypothetical prote
9	8	2.1	426	2 A10287	conserved hypotnet
10	8	2.1	503	2 A49432	activin receptor-1
11	8	2.1	555	2 T44010	virion protein (im
12	8	2.1	558	2 S57953	CABP protein alpha
13	7	1.8	42	2 A37896	progesterone recep
14	7	1.8	98	2 AE2201	hypothetical prote
15	7	1.8	106	2 AD0408	conserved hypotnet
16	7	1.8	115	2 AC1134	hypothetical prote
17	7	1.8	131	2 T22997	hypothetical prote
18	7	1.8	143	2 S47832	hypothetical 15.6K
19	7	1.8	143	2 A98190	hypothetical prote
20	7	1.8	143	2 B86037	hypothetical prote
21	7	1.8	147	2 S57440	hypothetical prote
22	7	1.8	156	1 NNHU1	lydb protein - pha
23	7	1.8	192	2 AH3643	pancreatic ribonuc
24	7	1.8	204	2 S52644	cytochrome b561 [i
25	7	1.8	211	2 A46458	phycobilisome matu
26	7	1.8	212	2 A81190	human CRI homolog
27	7	1.8	212	2 G81913	conserved hypotnet
28	7	1.8	219	2 A10886	hypothetical prote
29	7	1.8	222	2 AC2397	Deda-family integr
					ATP-binding protei

30	7	1.8	224	2 D83570	probable nucleotid
31	7	1.8	232	2 A82426	myoglobin ABC tra
32	7	1.8	243	2 S25755	Ig lambda chain -
33	7	1.8	243	2 A70670	hypothetical prote
34	7	1.8	261	2 B69095	coalt transport m
35	7	1.8	269	2 F8662	phosphonate ABC tr
36	7	1.8	272	2 G71618	merozoite surface
37	7	1.8	275	2 G69963	lipoprotein SpoIII
38	7	1.8	276	2 G64584	conserved hypotnet
39	7	1.8	283	2 B87546	acetoin dehydrogen
40	7	1.8	284	2 S27843	homeotic protein s
41	7	1.8	286	2 S08993	signal sequence re
42	7	1.8	286	2 I38246	signal sequence re
43	7	1.8	289	2 AD1354	oxidoreductase hom
44	7	1.8	291	2 A55980	opsin-related reti
45	7	1.8	291	2 I46965	G protein-coupled

ALIGNMENTS

RESULT 1
B26359
decay-accelerating factor, GPI-anchored splice form precursor - human
N:Alternate names: CD55; DAF splice form 2; decay-accelerating factor membrane-bound
C:Species: Homo sapiens (man)
C:Date: 05-Oct-1988 #sequence revision 16-Aug-1996 #text_change 19-Jan-2001
C:Accession: B26359; A27666; A39101; I52594; I52564
R:Caras, I.W.; Davitz, M.A.; Rhee, L.; Weddell, G.; Martin Jr., D.W.; Nussenzweig, V.
Nature 325, 545-549, 1987
A:Title: Cloning of decay-accelerating factor suggests novel use of splicing to gener
A:Reference number: A26359; MUID:87115845; PMID:2433596
A:Accession: B26359
A:Molecule type: mRNA
A:Residues: 1-381 <CAR>
A:Cross-references: GB:M50142; NID:g181464; PIDN:AAA52168.1; PID:g181465
R:Medoff, M.E.; Lublin, D.M.; Holers, V.M.; Ayers, D.J.; Getty, R.R.; Leykam, J.F.; At
Proc. Natl. Acad. Sci. U.S.A. 84, 2007-2011, 1987
A:Title: Cloning and characterization of cDNAs encoding the complete sequence of deca
A:Reference number: A27666; MUID:87175602; PMID:2436222
A:Accession: A27666
A:Molecule type: mRNA
A:Residues: 6-79, 'T', '81-84, 'M', '86-381 <MED>
A:Cross-references: GB:M15799; NID:g181462; PIDN:AAA52167.1; PID:g181463
R:Moran, P.; Raab, H.; Kohr, W.J.; Caras, I.W.
J. Biol. Chem. 266, 1250-1257, 1991
A:Title: Glycophospholipid membrane anchor attachment. Molecular analysis of the clea
A:Reference number: A39101; MUID:91093238; PMID:1824699
A:Accession: A39101
A:Molecule type: protein
A:Residues: 338-352 <MOR>
R:Lublin, D.M.; Mallinson, G.; Poole, J.; Reid, M.E.; Thompson, E.S.; Ferdman, B.R.;
Blood 84, 1276-1282, 1994
A:Title: Molecular basis of reduced or absent expression of decay-accelerating factor
A:Reference number: I52594; MUID:94325573; PMID:7519480
A:Accession: I52594
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 194-198, 'U', '200-209 <LUB>
A:Cross-references: GB:S72858; NID:G639599; PIDN:AAC60633.1; PID:G639600
A:Experimental source: Individual KW, Cromer blood group phenotype Dr(a-)
A:Note: the single nucleotide difference in this allele, which changes Ser-199 to Leu
on (see reference I52564), and thus reduced DAF expression
R:Reid, M.E.; Mallinson, G.; Slim, R.B.; Poole, J.; Fausch, V.; Merry, A.H.; Llew, Y.W
Blood 78, 3291-3297, 1991
A:Title: Biochemical studies on red blood cells from a patient with the Inab phenotyp
A:Reference number: I52564; MUID:92075980; PMID:1720702
A:Accession: I52564
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 190-193, 'Q' <CPVE' <RE2>
A:Cross-references: GB:S70688; NID:g240301; PIDN:AMB20576.1; PID:g240302
A:Experimental source: Individual KW, Cromer blood group phenotype Dr(a-) (described

C/Comment: Cromer blood group system antigens reside on this protein.
C/Comment: For an alternative splice form, see PIR:A26359.
C/Genetics:
A:Gene: GDB:DAF
A:Cross-references: GDB:119088; OMIM:125240
A:Map position: 1q32-1q32
C/Function:
A:Description: protects tissues from damage by regulating complement activation on cell
A:Superfamily: decay-accelerating factor; complement factor H repeat homology
C:Keywords: alternative splicing; blocked carboxyl end; complement inhibitor; glycoprotein
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-33/Product: decay-accelerating factor 2 #status predicted <MAT>
F:35-94/Domain: complement factor H repeat homology <FH01>
F:98-158/Domain: complement factor H repeat homology <FH02>
F:163-220/Domain: complement factor H repeat homology <FH03>
F:225-283/Domain: complement factor H repeat homology <FH04>
F:354-381/Domain: carboxyl-terminal propeptide #status predicted <PRO>
F:95/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:353/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form)

Query Match 100.0% Score 381; DB 1; Length 381;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVARPSVPALPLGLGELPRLLLVLLCLPAVWGDCGLPPVPAQALGRTSPEDTY 60
Db 1 MTVARPSVPALPLGLGELPRLLLVLLCLPAVWGDCGLPPVPAQALGRTSPEDTY 60
QY 61 IYKCESFVKIPGEKDSVLCCKGSDIEFCNRSCEVPTRLNSALQPYITQNYFP 120
Db 61 IYKCESFVKIPGEKDSVLCCKGSDIEFCNRSCEVPTRLNSALQPYITQNYFP 120
QY 121 VGVVVEECRPGYRREPSLSPKLTCLQNLKMTAVFECCKKSCNPGEIRNGQIDVPGGI 180
Db 121 VGVVVEECRPGYRREPSLSPKLTCLQNLKMTAVFECCKKSCNPGEIRNGQIDVPGGI 180
QY 181 LFGATISFSCNTGKILFGSTSSFCILSGSSVQSDPLPECREIYCPAPPOIDNGIIOGER 240
Db 181 LFGATISFSCNTGKILFGSTSSFCILSGSSVQSDPLPECREIYCPAPPOIDNGIIOGER 240
QY 241 DHGYSRQSVTYACNKGFTMGHSIYCTVNNDEGMSGPPECRGKSLTSKVPYQKPT 300
Db 241 DHGYSRQSVTYACNKGFTMGHSIYCTVNNDEGMSGPPECRGKSLTSKVPYQKPT 300
QY 301 TVVAVPTTEVSPISQKTTKTTPNAQATRSTPVSRTHKHETTPKNGSGTSTGTRLLS 360
Db 301 TVVAVPTTEVSPISQKTTKTTPNAQATRSTPVSRTHKHETTPKNGSGTSTGTRLLS 360
QY 361 GHTCFTLTGLGLTVMGLLT 381
Db 361 GHTCFTLTGLGLTVMGLLT 381

RESULT 2
A26359
decay-accelerating factor, splice form 1 precursor - human
N:Alternate names: decay-accelerating factor 5; decay-accelerating factor secreted form
C:Species: Homo sapiens (man)
C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 02-Jun-2000
C:Accession: A26359; A39702; S16187; S23138; A27258
R:Carls, I.W.; Davitz, M.A.; Rhee, L.; Weddell, G.; Martin Jr., D.W.; Nussenzweig, V.
Nature 325, 545-549, 1987
A:Title: Cloning of decay-accelerating factor suggests novel use of splicing to generate
A:Reference number: A26359; MUID:87115845; PMID:2433596
A:Accession: A26359
A:Molecule type: mRNA
A:Residues: 1-440 <CR>
A:Cross-references: GB:M30142
R:Emulonu, U.K.; Ravi, L.; Medof, M.E.
Proc Natl. Acad. Sci. U.S.A. 86, 4675-4679, 1991
A:Title: Characterization of the decay-accelerating factor gene promoter region.
A:Reference number: A39702; MUID:91271256; PMID:1711208
A:Accession: A39702

A:Molecule type: DNA
A:Residues: 179,'T',81-104 <EMD>
A:Cross-references: GB:M64356
A:Note: The authors translated the codon AGT for residue 85 as Met
R:Nakano, Y.; Sugita, Y.; Ishikawa, Y.; Choi, N.H.; Tobe, T.; Tomita, M.
Biochim. Biophys. Acta 1074, 326-330, 1991
A:Title: Isolation of two forms of decay-accelerating factor (DAF) from human urine.
A:Reference number: S16187; MUID:91291869; PMID:1712233
A:Accession: S16187
A>Status: preliminary
A:Molecule type: protein
A:Residues: 35-47 <R10>
R:Nakano, Y.; Sunida, K.; Kikuta, N.; Miura, N.H.; Tobe, T.; Tomita, M.
Biochim. Biophys. Acta 1116, 235-240, 1992
A:Title: Complete determination of disulfide bonds localized within the short consens
A:Reference number: S23138; MUID:92305034; PMID:1377029
A:Accession: S23138
A>Status: preliminary
A:Molecule type: protein
A:Residues: 35-41;65-68;79-81;93-103;128-134;143-145;155-159;162-168;188-192;203-204;
R:Sugita, Y.; Negoro, T.; Matsuda, T.; Sakamoto, T.; Tomita, M.
J. Biochem. 100, 143-150, 1986
A:Title: Improved method for the isolation and preliminary characterization of human
A:Reference number: A27258; MUID:87008461; PMID:2428813
A:Accession: A27258
A:Molecule type: protein
A:Residues: 35,'X',37,'G',39-51,'P',53-55,'X',57-58,'X',60-63 <SUG>
A:Note: gly-35 and leu-38 were also found
C/Comment: For an alternative splice form, see PIR:B26359
C/Genetics:
A:Gene: GDB:DAF
A:Cross-references: GDB:119088; OMIM:125240
A:Map position: 1q32-1q32
A:Superfamily: decay-accelerating factor; complement factor H repeat homology
C:Keywords: alternative splicing; glycoprotein
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-44/Product: decay-accelerating factor 1 #status predicted <MAT>
F:36-94/Domain: complement factor H repeat homology <FH01>
F:98-158/Domain: complement factor H repeat homology <FH02>
F:163-220/Domain: complement factor H repeat homology <FH03>
F:225-283/Domain: complement factor H repeat homology <FH04>
F:95/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 94.8% Score 361; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVARPSVPALPLGLGELPRLLLVLLCLPAVWGDCGLPPVPAQALGRTSPEDTY 60
Db 1 MTVARPSVPALPLGLGELPRLLLVLLCLPAVWGDCGLPPVPAQALGRTSPEDTY 60
QY 61 IYKCESFVKIPGEKDSVLCCKGSDIEFCNRSCEVPTRLNSALQPYITQNYFP 120
Db 61 IYKCESFVKIPGEKDSVLCCKGSDIEFCNRSCEVPTRLNSALQPYITQNYFP 120
QY 121 VGVVVEECRPGYRREPSLSPKLTCLQNLKMTAVFECCKKSCNPGEIRNGQIDVPGGI 180
Db 121 VGVVVEECRPGYRREPSLSPKLTCLQNLKMTAVFECCKKSCNPGEIRNGQIDVPGGI 180
QY 181 LFGATISFSCNTGKILFGSTSSFCILSGSSVQSDPLPECREIYCPAPPOIDNGIIOGER 240
Db 181 LFGATISFSCNTGKILFGSTSSFCILSGSSVQSDPLPECREIYCPAPPOIDNGIIOGER 240
QY 241 DHGYSRQSVTYACNKGFTMGHSIYCTVNNDEGMSGPPECRGKSLTSKVPYQKPT 300
Db 241 DHGYSRQSVTYACNKGFTMGHSIYCTVNNDEGMSGPPECRGKSLTSKVPYQKPT 300
QY 301 TVVAVPTTEVSPISQKTTKTTPNAQATRSTPVSRTHKHETTPKNGSGTSTGTRLLS 360
Db 301 TVVAVPTTEVSPISQKTTKTTPNAQATRSTPVSRTHKHETTPKNGSGTSTGTRLLS 360
QY 361 G 361

Db 361 G 361

RESULT 3

156234
decay-accelerating factor - orangutan (fragment)
C:Species: Pongo pygmaeus (orangutan)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C:Accession: 156234
R:Nickells, M.W.; Alvarez, J.I.; Lublin, D.M.; Atkinson, J.P.
J. Immunol. 152, 676-685, 1994
A:Title: Characterization of DAF-2, a high molecular weight form of decay-accelerating factor
A:Reference number: 156234; MUID:94110622; PMID:7506731
A:Accession: 156234
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-340 <RES>
A:Cross-references: GB:567775; NID:9459389; PIDN:AAC0609.1; PID:9459390
C:Superfamily: decay-accelerating factor; complement factor H repeat homology
F:1-53/Domain: complement factor H repeat homology (fragment) <FH01>
F:57-117/Domain: complement factor H repeat homology <FH02>
F:122-119/Domain: complement factor H repeat homology <FH03>
F:184-242/Domain: complement factor H repeat homology <FH04>

Query Match 22.3%; Score 85; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.4e-76;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 272 DEGEISGPPPCRCRGSLSLTKVPYQKRTYVNPPTTEVSPTSQKTTTTPNMAQATST 331

Db 231 DEGEISGPPPCRCRGSLSLTKVPYQKRTYVNPPTTEVSPTSQKTTTTPNMAQATST 290

Qy 332 PVSRTTKHFHETTPKNGSGTSGTT 356

Db 291 PVSRTTKHFHETTPKNGSGTSGTT 315

RESULT 4

NBHU

apolipoprotein H precursor [validated] - human

N:Alternate names: activated protein C-binding protein; antidiolipin cofactor; beta-2

C:Species: Homo sapiens (man)

C:Date: 17-May-1995 #sequence_revision 30-Jun-1993 #text_change 08-Dec-2000

C:Accession: S17178; S17668; J01379; B43286; A03209; A46464; I54745; S15499; S20

R:Steinmasser, A.; Estallier, C.; Weiss, E.H.; Sim, R.B.; Day, A.J.

Biochem. J. 277, 387-391, 1991

A:Title: Complete nucleotide and deduced amino acid sequence of human beta(2)-glycoprote

A:Reference number: S17178; MUID:91315408; PMID:1650181

A:Accession: S17178

A:Molecule type: mRNA

A:Residues: 1-345 <RES>

A:Cross-references: EMBL:X58100; NID:928809; PIDN:CA44113.1; PID:928810

R:Kristensen, T.; Schousboe, I.; Boel, E.; Mulvihill, E.M.; Rosendahl Hansen, R.; Bach M

FEBS Lett. 289, 183-186, 1991

A:Title: Molecular cloning and mammalian expression of human beta(2)-glycoprotein I CDNA

A:Reference number: S17668; MUID:92008618; PMID:1655523

A:Accession: S17668

A:Molecule type: mRNA

A:Residues: 1-345 <KRI>

A:Cross-references: EMBL:X53595; NID:928811; PIDN:CA437664.1; PID:928812

R:Mehdi, H.; Nunn, M.; Steel, D.M.; Whitehead, A.S.; Perez, M.; Walker, L.; Peeples, M.E

Gene 108, 293-298, 1991

A:Title: Nucleotide sequence and expression of the human gene encoding apolipoprotein H

A:Reference number: J01379; MUID:92084151; PMID:1748314

A:Accession: J01379

A:Molecule type: mRNA

A:Residues: 1-265, 'V', 267-345 <MEH>

A:Cross-references: EMBL:X57847; NID:928813; PIDN:CA440977.1; PID:928814

R:Nonaka, M.; Matsuda, Y.; Shiroishi, T.; Motiwaki, K.; Nonaka, M.; Natsume-Sakai, S.

Genomics 13, 1082-1087, 1992
A:Title: Molecular cloning of mouse beta-2-glycoprotein I and mapping of the gene to chr

A:Reference number: A43286; MUID:92372000; PMID:1339387

A:Accession: B43286
A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-265, 'V', 267-345 <NON>

R:Lozier, J.; Takahashi, N.; Putnam, F.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 3640-3644, 1984

A:Title: Complete amino acid sequence of human plasma beta2-glycoprotein I.

A:Reference number: A03209; MUID:84222015; PMID:6587378

A:Accession: A03209

A:Molecule type: protein

A:Residues: 20-120, 'C', 122-187, 'N', 189-265, 'V', 267-345 <LOZ>

R:McNeill, H.P.; Simpson, R.J.; Chesterman, C.N.; Killis, S.A.

Proc. Natl. Acad. Sci. U.S.A. 87, 4120-4124, 1990

A:Title: Anti-phospholipid antibodies are directed against a complex antigen that inc

A:Reference number: A35786; MUID:90272666; PMID:2349221

A:Accession: A35786

A:Molecule type: protein

A:Residues: 20-22, 'X', 24-37, 'X', 39-43 <MCN>

R:Matsura, E.; Igarashi, Y.; Fujimoto, M.; Ichikawa, K.; Suzuki, T.; Sumida, T.; Yas

J. Immunol. 148, 3885-3891, 1992

A:Title: Heterogeneity of antidiolipin antibodies defined by the antidiolipin c

A:Reference number: A46464; MUID:92291509; PMID:1602135

A:Accession: A46464

A:Molecule type: protein

A:Residues: 20-44 <MA2>

A:Note: sequence extracted from NCBI backbone (NCBI:105524)

R:Matsura, E.; Igarashi, M.; Igarashi, Y.; Nage, H.; Ichikawa, K.; Yasuda, T.; Kolk

Int. Immunol. 3, 1217-1221, 1991

A:Title: Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by cDNA clo

A:Reference number: I54745; MUID:92135065; PMID:1777418

A:Accession: I54745

A:Status: preliminary; translated from GR/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-265, 'V', 267-345 <RES>

A:Cross-references: GB:S80305; NID:9244677; PIDN:ABR21330.1; PID:9244678

C:Comment: This plasma glycoprotein is a constituent of chylomicrons, VLDL, and HDL.

C:Blood coagulation cascade and ADP-mediated platelet aggregation.

C:Comment: The physiological role of this protein is uncertain. It may diminish unwar

C:Genetics:

A:Gene: GDB:AP0H

A:Cross-references: GDB:118887; OMIM:138700

A:Map position: 19q23-17qter

C:Superfamily: apolipoprotein H; complement factor H repeat homology

C:Keywords: chylomicron; duplication; glycoprotein; HDL; heparin binding; lipid bindi

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-345/Product: apolipoprotein H #status experimental <MAT>

F:23-79/Domain: complement factor H repeat homology <FH1>

F:84-137/Domain: complement factor H repeat homology <FH2>

F:142-200/Domain: complement factor H repeat homology <FH3>

F:205-260/Domain: complement factor H repeat homology <FH4>

F:264-325/Domain: complement factor H repeat homology <FH5>

F:23-66, 51-79, 110-137, 174-200, 205-248, 300-307/Disulfide bonds: #status experimental

F:84-124, 142-188, 234-260, 264-315, 335-345/Disulfide bonds: #status predicted

F:162, 183, 193, 253/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 2.4%; Score 9; DB 1; Length 345;

Best Local Similarity 100.0%; Pred. No. 1.2;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 TISFSCNTG 193

Db 105 TISFSCNTG 113

RESULT 5

150726
cation-independent mannose-6-phosphate receptor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999

C:Accession: I50726

R:Zhou, M.; Ma, Z.; Sly, W.S.

Proc. Natl. Acad. Sci. U.S.A. 92, 9762-9766, 1995

A:Title: Cloning and expression of the cDNA of chicken cation-independent mannose-6-p

A:Reference number: I50726; MUID:96003859; PMID:7568213
 A:Accession: I50726
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-2470 <RH0>
 A:Cross-references: EMBL:U55037; NID:91019118; PIDN:AMC59718.1; PID:91019119
 C:Superfamily: mannose 6-phosphate receptor, cation-independent; fibronectin type II ref F:1882-1921/Domain: fibronectin type II repeat homology <2FI>

Query Match 2.4%; Score 9; DB 2; Length 2470;
 Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 22 LLVLVLCIP 30
 9 LLVLVLCIP 17

RESULT 6

D83295
 transaldolase PA2796 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: D83295
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Llm,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: D83295
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-307 <STO>
 A:Cross-references: GB:AE004707; GB:AE004091; NID:99948876; PIDN:AAG06184.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: tal; PA2796
 C:Superfamily: human transaldolase

Query Match 2.1%; Score 8; DB 2; Length 307;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GELPRILL 23
 Db 249 GELPRILL 256

RESULT 7

G75283
 asparaginase (EC 3.5.1.1) [similarity] - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
 C:Accession: G75283
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: G75283
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-347 <WHI>
 A:Cross-references: GB:AE002066; GB:AE000513; NID:96460163; PIDN:AAF1189.1; PID:9646016
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2353
 A:Map position: 1
 C:Superfamily: asparaginase
 C:Keywords: hydrolase

Query Match 2.1%; Score 8; DB 2; Length 347;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 RLILVLL 27
 Db 322 RLILVLL 329

RESULT 8

H75628
 hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: H75628
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
 .; M.; Shen, M.; Yamathavan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: H75628
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-413 <WHI>
 A:Cross-references: GB:AE001826; NID:96460827; PIDN:AAF12617.1; PID:96460913; TIGR:DR
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DRB0098
 A:Map position: megaplasmid
 A:Genome: plasmid
 A:Note: plasmid MPI

Query Match 2.1%; Score 8; DB 2; Length 413;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLIGELP 19
 Db 27 LPLIGELP 34

RESULT 9

AI0287
 conserved hypothetical protein YPO2360 [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
 C:Accession: AI0287
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tilball, R.W.; Holden, M.T.G.; Prentice, M
 deno-Iarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
 Nature 413, 523-527, 2001
 A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AI0287
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-426 <XUR>
 A:Cross-references: GB:AL590842; PIDN:CAC91165.1; PID:g15980357; GSPDB:GN00175
 C:Genetics:
 A:Gene: YPO2360
 C:Superfamily: Escherichia coli probable membrane protein yciW

Query Match 2.1%; Score 8; DB 2; Length 426;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 TTVNVPTT 307
 Db 34 TTVNVPTT 41

RESULT 10

A49432
activin receptor-like kinase 5 precursor - human
C:Accession: S57953
N:Alternate names: TGFbeta type I receptor ALK-5
N:Contains: protein kinase (man)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C:Accession: A49432
R:Franzen, P.; ten Dijke, P.; Ichijo, H.; Yamashita, H.; Schultz, P.; Heldin, C.H.; Miyaz
Cell 75, 681-692, 1993
A:Title: Cloning of a TGFbeta type I receptor that forms a heteromeric complex with the
A:Reference number: A49432; MUID:94061986; PMID:8242743
A:Accession: A49432
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-503 <FRA>
A:Cross-references: GB:L11695; NID:9431034; PIDN:AAA16073.1; PID:9431035
C:Superfamily: unassigned Ser/thr or Tyr-specific protein kinases; protein kinase homol
C:Keywords: ATP; glycoprotein; phosphotransferase; transmembrane protein
F:203-499/Domain: protein kinase homology <KIN>
F:211-219/Region: protein kinase ATP-binding motif

Query Match 2.1%; Score 8; DB 2; Length 503;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 PRLLTLVL 26
|||||||
Db 10 PRLLTLVL 17

RESULT 11

T44010
varion protein [imported] - human herpesvirus 6
C:Species: human herpesvirus 6
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44010; T44197
R:Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kaw
J. Virol. 73, 8053-8063, 1999
A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and
A:Reference number: 222732; MUID:99412319; PMID:10482554
A:Accession: T44010
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-555 <ISE>
A:Cross-references: EMBL:AB021506; NID:9495977; PIDN:BA78271.1; PID:9496038
A:Experimental source: strain HST; pop. variant B
R:Dominguez, G.; Dambugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1999
A:Title: Human herpesvirus 6B genome sequence: coding content and comparison with human
A:Reference number: 222734; MUID:99412318; PMID:10482553
A:Accession: T44197
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-555 <DOM>
A:Cross-references: EMBL:AF157706; PIDN:AAB06348.1
A:Experimental source: strain 229; variant B
C:Genetics:
A:Gene: US0
C:Superfamily: varicella-zoster virus gene 34 protein

Query Match 2.1%; Score 8; DB 2; Length 555;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 71 KIPGEKDS 78
|||||||
Db 311 KIPGEKDS 318

RESULT 12

S57953
C4BP protein alpha chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)

C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
C:Accession: S57953
R:Hillard, A.; Thern, A.; Dahlback, B.
submitted to the EMBL Data Library, July 1995
A:Description: Molecular cloning of rat C4b-binding protein alpha- and beta-chains: s
A:Reference number: S57953
A:Accession: S57953
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-558 <HIL>
A:Cross-references: EMBL:Z50051; NID:9899379; PIDN:CAA90391.1; PID:9899380
C:Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology
F:15-72/Domain: complement factor H repeat homology <FH1>
F:77-134/Domain: complement factor H repeat homology <FH2>
F:139-199/Domain: complement factor H repeat homology <FH3>
F:204-258/Domain: complement factor H repeat homology <FH4>
F:263-324/Domain: complement factor H repeat homology <FH5>
F:328-386/Domain: complement factor H repeat homology <FH6>
F:390-443/Domain: complement factor H repeat homology <FH7>
F:447-501/Domain: complement factor H repeat homology <FH8>

Query Match 2.1%; Score 8; DB 2; Length 558;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 213 WSDPLEPC 220
|||||||
Db 127 WSDPLEPC 134

RESULT 13

A37896
progesterone receptor - chicken (fragments)
C:Species: Gallus gallus (chicken)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 31-Oct-1997
C:Accession: A37896
R:Denner, L.A.; Schrader, W.T.; O'Malley, B.W.; Wigel, N.L.
J. Biol. Chem. 265, 16548-16555, 1990
A:Title: Hormonal regulation and identification of chicken progesterone receptor phos
A:Reference number: A37896; MUID:90375528; PMID:2398063
A:Accession: A37896
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-42 <DEN>
C:Superfamily: progesterone receptor; erba transforming protein homology
C:Keywords: steroid hormone receptor; zinc finger

Query Match 1.8%; Score 7; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 PVPVPAAL 12
|||||||
Db 29 PVPVPAAL 35

RESULT 14

AE2201
hypothetical protein asj1164 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AE2201
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2201
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA874863.1; PID:917132259; GSPDB:GN00179

A:Experimental source: strain FCC 7120
 C:Genetics:
 A:Gene: asl3164

Query Match 1.8%; Score 7; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 LLLLVLL 27
 |||||
 Db 29 LLLLVLL 35

RESULT 15

AD0408
 conserved hypothetical protein YP03362 [Imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
 C:Accession: AD0408
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, H.
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AD0408
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-106 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CAC92592.1; PID:g15981289; GSPDB:GN00175
 C:Genetics:
 A:Gene: YP03362
 C:Superfamily: hypothetical protein HI0673

Query Match 1.8%; Score 7; DB 2; Length 106;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 LLLLVLL 27
 |||||
 Db 6 LLLLVLL 12

Search completed: February 12, 2003, 11:11:57
 Job time : 25 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:10:31 ; Search time 13 Seconds
(without alignments)
748.779 Million cell updates/sec

Title: US-09-623-035-2

Perfect score: 381
Sequence: 1 MTVARPSVPAALPLGLR.....HTCFTLLGLLTWTMLLT 381

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 140259 seqs, 25548876 residues

Word size : 0

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	17.1	182	10	US-09-925-299-1141
2	37	9.7	37	8	US-08-873-601-12
3	37	9.7	37	9	US-09-792-630-65
4	37	9.7	37	9	US-10-080-376-65
5	37	9.7	37	9	US-10-061-395-13
6	37	9.7	37	9	US-10-096-339-12
7	37	9.7	37	10	US-09-157-748-19
8	37	9.7	37	10	US-09-166-940-16
9	37	9.7	37	10	US-09-922-503-9
10	37	9.7	37	10	US-09-925-664-27
11	37	9.7	37	9	US-09-925-664-30
12	23	6.0	41	10	US-09-729-835-125
13	10	2.6	263	10	US-09-800-729-88
14	10	2.6	372	10	US-09-800-729-213
15	9	2.4	345	9	US-09-924-340-106
16	9	2.4	345	9	US-09-992-600A-106
17	8	2.1	503	10	US-09-903-068-10
18	7	1.8	34	10	US-09-864-761-43063
19	7	1.8	71	10	US-09-864-761-47821

20	7	1.8	86	10	US-09-764-860-544	Sequence 544, App
21	7	1.8	140	10	US-09-864-761-42549	Sequence 42549, A
22	7	1.8	155	10	US-09-925-297-504	Sequence 504, App
23	7	1.8	184	10	US-09-729-674-32	Sequence 32, App
24	7	1.8	184	10	US-09-925-297-737	Sequence 737, App
25	7	1.8	209	10	US-09-893-737-126	Sequence 126, App
26	7	1.8	224	9	US-09-975-719-175	Sequence 175, App
27	7	1.8	226	9	US-09-859-211-35	Sequence 35, App
28	7	1.8	230	9	US-10-063-547-60	Sequence 60, App
29	7	1.8	230	9	US-10-028-072-492	Sequence 492, App
30	7	1.8	230	9	US-10-063-616-80	Sequence 80, App
31	7	1.8	230	9	US-10-063-502-80	Sequence 80, App
32	7	1.8	230	9	US-10-121-049-492	Sequence 492, App
33	7	1.8	230	9	US-10-123-904-492	Sequence 492, App
34	7	1.8	230	9	US-10-140-470-492	Sequence 492, App
35	7	1.8	230	9	US-10-175-746-492	Sequence 492, App
36	7	1.8	230	9	US-10-176-921-492	Sequence 492, App
37	7	1.8	230	9	US-10-176-921-492	Sequence 492, App
38	7	1.8	230	10	US-09-949-192-35	Sequence 35, App
39	7	1.8	230	10	US-09-998-598-2590	Sequence 2590, App
40	7	1.8	230	12	US-10-006-867-80	Sequence 80, App
41	7	1.8	261	10	US-09-925-297-532	Sequence 532, App
42	7	1.8	276	9	US-09-895-913A-356	Sequence 356, App
43	7	1.8	297	10	US-09-925-302-609	Sequence 609, App
44	7	1.8	345	10	US-09-401-636-10	Sequence 10, App
45	7	1.8	347	10	US-09-886-055-155	Sequence 155, App

ALIGNMENTS

RESULT 1
US-09-925-299-1141
Sequence 1141, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1141
LENGTH: 182
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (123)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (126)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (128)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (137)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (143)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (157)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (163)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE
LOCATION: (165)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (176)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1141

Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e-50; Length 182;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 EHSIYCVNDEGEMSGPPPECKRSKLSKYPTVOKPTVNVPTTEVSPTSKTTTKT 321
DB 3 EHSIYCVNDEGEMSGPPPECKRSKLSKYPTVOKPTVNVPTTEVSPTSKTTTKT 62

QY 322 TPNAQ 326
DB 63 TPNAQ 67

RESULT 2
US-08-873-601-12
Sequence 12, Application US/08873601
Patent No. US20020064798A1
GENERAL INFORMATION:

APPLICANT: No. US20020064798A1an, Garry P.
TITLE OF INVENTION: COMBINATORIAL ENZYMAIC COMPLEXES
FILE REFERENCE: A-63915/DJB/RMS
CURRENT APPLICATION NUMBER: US/08/873,601
CURRENT FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 37
TYPE: PRT
ORGANISM: Unknown
FEATURE:

OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
US-08-873-601-12

Query Match
Best Local Similarity 100.0%; Pred. No. 6.5e-26; Length 37;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 381
DB 1 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 37

RESULT 3
US-09-792-630-65
Sequence 65, Application US/09792630
Patent No. US20020168640A1
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: BIOCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES
FILE REFERENCE: A-70295/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/792,630
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.1
SEQ ID NO 65
LENGTH: 37
TYPE: PRT
ORGANISM: Rattus sp.
US-09-792-630-65

Query Match
Best Local Similarity 100.0%; Pred. No. 6.5e-26; Length 37;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 381
DB 1 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 37

RESULT 4
US-10-080-376-65
Sequence 65, Application US/10080376
Patent No. US20020172968A1
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: BIOCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES
FILE REFERENCE: A-70295-2/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/080,376
CURRENT FILING DATE: 2000-02-19
PRIOR APPLICATION NUMBER: US 09/792,630
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.1
SEQ ID NO 65
LENGTH: 37
TYPE: PRT
ORGANISM: Rattus sp.
US-10-080-376-65

Query Match
Best Local Similarity 100.0%; Pred. No. 6.5e-26; Length 37;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 381
DB 1 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 37

RESULT 5
US-10-061-395-13
Sequence 13, Application US/10061395
Publication No. US20020192675A1
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: Methods of Identifying Regulator Molecules
FILE REFERENCE: 1821.0080003
CURRENT APPLICATION NUMBER: US/10/061,395
CURRENT FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/271,423
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/265,880
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/265,589
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DAF GPI anchor
US-10-061-395-13

Query Match
Best Local Similarity 100.0%; Pred. No. 6.5e-26; Length 37;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 381
DB 1 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 37

RESULT 6

US-10-096-339-12
; Sequence 12, Application US/10096339
; Publication No. US20030022196A1
; GENERAL INFORMATION:
; APPLICANT: Lorens, James B.
; APPLICANT: Kinsella, Todd
; APPLICANT: Masuda, Esteban
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Liao, X. Charlene
; APPLICANT: Pearisall, Denise
; APPLICANT: Freira, Annabelle
; APPLICANT: Chu, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING FOR ALTERED CELLULAR PHENO
; FILE REFERENCE: A-71158/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/096,339
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 09/076,624
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-096-339-12

Query Match 9.7%; Score 37; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 345 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 381
DB 1 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 37

RESULT 7
US-09-157-748-19
; Sequence 19, Application US/09157748
; Patent No. US20010003042A1
; GENERAL INFORMATION:
; APPLICANT: Lorens, James
; TITLE OF INVENTION: MULTIPARAMETER FACs Assays to Detect Alterations in
; FILE REFERENCE: A66587/DJB/RMS
; CURRENT APPLICATION NUMBER: US/09/157,748
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; JOURNAL: Nature
; VOLUME: 333
; ISSUE: 6170
; PAGES: 269-272
; DATE: 1988
; PUBLICATION INFORMATION:
; JOURNAL: J. Biol. Chem.
; VOLUME: 266
; PAGES: 1250-
; DATE: 1991
US-09-157-748-19

Query Match 9.7%; Score 37; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 345 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 381
DB 1 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 37

RESULT 8
US-09-916-940-16
; Sequence 16, Application US/09916940
; Patent No. US20020127564A1
; GENERAL INFORMATION:
; APPLICANT: NO. US20020127564Alan, Garry P
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; FILE REFERENCE: A-64260-6/RMS/AMS
; CURRENT APPLICATION NUMBER: US/09/916,940
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 09/727,715
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 08/963,368
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: US 08/589,109
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: US 08/589,911
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: US 08/789,333
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 08/787,738
; PRIOR FILING DATE: 1997-01-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: membrane
US-09-916-940-16

Query Match 9.7%; Score 37; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 345 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 381
DB 1 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 37

RESULT 9
US-09-922-503-9
; Sequence 9, Application US/09922503
; Patent No. US20020137022A1
; GENERAL INFORMATION:
; APPLICANT: Li, Min
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE CONSTRUCTION AND USE OF ENVEL
; FILE REFERENCE: A-69633-1/RT/RMS/RWK
; CURRENT APPLICATION NUMBER: US/09/922,503
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/222,697
; PRIOR FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-922-503-9

Query Match 9.7%; Score 37; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.5e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 345 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 381
DB 1 PNKSGTSGTTRLLSGHTCFTLGLGLTVMGLLT 37

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RESULT 10
US-09-925-664-27
: Sequence 27, Application US/09925664
: Patent No. US2002016006A1
: GENERAL INFORMATION:
: APPLICANT: Denney, Jr., Dan W.
: TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
: FILE REFERENCE: GENIPOPE-06499
: CURRENT APPLICATION NUMBER: US/09/925,664
: CURRENT FILING DATE: 2001-08-09
: PRIOR APPLICATION NUMBER: 09/370,453
: PRIOR FILING DATE: 1999-08-09
: PRIOR APPLICATION NUMBER: 08/644,664
: PRIOR FILING DATE: 1996-05-01
: PRIOR APPLICATION NUMBER: 08/761,277
: PRIOR FILING DATE: 1996-12-06
: NUMBER OF SEQ ID NOS: 80
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 27
: LENGTH: 248
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic
US-09-925-664-27

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Query Match	9.7%	Score 37;	DB 9;	Length 248;
Best Local Similarity	100.0%	Pred. No. 3.4e-25;		
Matches	37;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
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Db	212	PNKSGTTSGLTRLSGATCFLLTGTLVMSGLT	248	

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RESULT 11
US-09-925-664-30
; Sequence 30, Application US/09925664
; Patent No. US2002016006A1
; GENERAL INFORMATION:
; APPLICANT: Denney, Jr., Dan W.
; TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
; FILE REFERENCE: GENITOPE-06499
; CURRENT APPLICATION NUMBER: US/09/925,664
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/370,453
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: 08/644,664
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/761,277
; PRIOR FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: patentIn version 3.1
; SEQ ID NO 30
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-925-664-30

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Query Match          9.7%; Score 37; DB 9; Length 261;
Best Local Similarity 100.0%; Pident. No. 3.5e-25;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 345 P N K G S G T T S G T T R L L S G H T C F T T L G L A T I V M G L L T 381
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 225 P N K G S G T T S G T T R L L S G H T C F T T L G L A T I V M G L L T 261

RESULT 12
US-09-729-835-125

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Sequence 125, Application US/09729835
Patent No. US2001001647A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 29 Human Secreted Proteins
FILE REFERENCE: P2015P1
CURRENT APPLICATION NUMBER: US/09/729,835
CURRENT FILING DATE: 2000-12-06
PRIORITY APPLICATION NUMBER: 09/257,179
PRIORITY FILING DATE: 1999-02-25
PRIORITY APPLICATION NUMBER: 60/056,270
PRIORITY FILING DATE: 1997-08-29
PRIORITY APPLICATION NUMBER: 60/056,271
PRIORITY FILING DATE: 1997-08-29
PRIORITY APPLICATION NUMBER: 60/056,247
PRIORITY FILING DATE: 1997-08-29
PRIORITY APPLICATION NUMBER: 60/056,073
PRIORITY FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 125
LENGTH: 41
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (34)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-729-835-125

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Query Match          6.0%; Score 23; DB 10; Length 41;  
Best Local Similarity 100.0%; Pred. No. 1-6e-13;  
Matches    23; Conservative    0; Mismatches    0; Indels    0;  
  
QY   194 YKLFGSTSFCLISGSSVQWSDP 216  
      |||||||||  
Db    11 YKLFGSTSFCLISGSSVQWSDP 33
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```

RESULT 13
US-09-800-729-88
? Sequence 88, Application US/09800729
? Patent No. US20020068319A1
? GENERAL INFORMATION:
? APPLICANT: N1 et al..
? TITLE OF INVENTION: 32 Human secreted proteins
? FILE REFERENCE: P204P1
? CURRENT APPLICATION NUMBER: US/09/800,729
? CURRENT FILING DATE: 2001-03-08
? PRIOR APPLICATION NUMBER: PCT/US00/26013
? PRIOR FILING DATE: 2000-09-22
? PRIOR APPLICATION NUMBER: 60/155,709
? PRIOR FILING DATE: 1999-09-24
? NUMBER OF SEQ ID NOS: 217
? SOFTWARE: Patentln Ver. 2.0
? SEQ ID NO 88
? LENGTH: 263
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (27)
? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
? NAME/KEY: SITE
? LOCATION: (112)
? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-800-729-88

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Query Match	2.6%	Score 10:	DB 10;	Length 263;
Best Local Similarity	100.0%;	Pred. No. 0.23;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0.
0Y	124	WVEYECRPGY	133	

Db 118 VVEYECRPGY 127

RESULT 14

US-09-800-729-213
; Sequence 213, Application US/09800729
; Patent No. US20020068319A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800/729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 213
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-213

Query Match

2.6%; Score 9; DB 10; Length 372;

Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 VVEYECRPGY 133

Db 118 VVEYECRPGY 127

RESULT 15

US-09-924-340-106
; Sequence 106, Application US/09924340
; Publication No. US20030027248A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephanie
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDMS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US2.REG
; CURRENT APPLICATION NUMBER: US/09/924,340
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 106
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..19
US-09-924-340-106

Query Match

2.4%; Score 9; DB 9; Length 345;

Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 185 TISFSCNTG 193

Db 105 TISFSCNTG 113

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:09:46 ; Search time 16 Seconds
(without alignments)
700.633 Million cell updates/sec

Title: US-09-623-035-2

Perfect score: 381
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4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/CTUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	323	84.8	323	2	US-08-435-149-2
2	323	84.8	577	2	US-08-435-149-3
3	323	84.8	611	4	US-09-475-460A-32
4	323	84.8	611	4	US-09-748-061A-32
5	273	71.7	324	1	US-08-310-416A-14
6	273	71.7	324	2	US-08-888-171-14
7	128	33.6	128	6	US14582-42
8	37	9.7	37	4	US-08-789-333F-16
9	37	9.7	37	4	US-09-133-944-16
10	37	9.7	37	4	US-09-208-827-17
11	37	9.7	37	4	US-08-787-738B-16
12	37	9.7	37	4	US-09-157-748-19
13	37	9.7	42	1	US-08-004-492-4
14	37	9.7	42	1	US-08-004-492-7
15	37	9.7	102	1	US-08-282-951-2
16	37	9.7	248	2	US-08-644-664B-27
17	37	9.7	248	2	US-08-761-277A-27
18	37	9.7	261	1	US-08-644-664B-30
19	37	9.7	261	2	US-08-761-277A-30
20	37	9.7	272	1	US-08-282-951-6
21	29	7.6	36	4	US-09-169-015-26
22	23	6.0	41	4	US-09-257-179-125
23	22	5.8	23	1	US-07-811-048-8
24	9	2.4	128	6	US14582-34
25	9	2.4	181	2	US-08-640-977-3
26	9	2.4	248	2	US-08-640-977-2
27	9	2.4	266	2	US-08-640-977-4

28	9	2.4	326	2	US-08-640-977-1	Sequence 1, Appl1
29	8	2.1	8	1	US-08-210-266A-4	Sequence 4, Appl1
30	8	2.1	8	1	US-08-688-675-4	Sequence 4, Appl1
31	8	2.1	8	3	US-08-477-860C-4	Sequence 2, Appl1
32	8	2.1	363	4	US-09-382-256-10	Sequence 10, Appl1
33	8	2.1	503	4	US-09-395-115-10	Sequence 10, Appl1
34	8	2.1	503	4	US-08-436-265-10	Sequence 10, Appl1
35	8	2.1	503	4	US-08-679-187-10	Sequence 10, Appl1
36	8	2.1	503	4	US-08-210-266A-5	Sequence 5, Appl1
37	7	1.8	7	1	US-08-688-675-5	Sequence 5, Appl1
38	7	1.8	7	3	US-08-477-860C-5	Sequence 16, Appl1
39	7	1.8	23	2	US-08-652-450A-16	Sequence 10, Appl1
40	7	1.8	60	1	US-08-210-266A-10	Sequence 10, Appl1
41	7	1.8	60	3	US-08-688-675-10	Sequence 10, Appl1
42	7	1.8	60	3	US-08-477-860C-10	Sequence 10, Appl1
43	7	1.8	89	4	US-09-134-001C-4553	Sequence 194, App
44	7	1.8	109	4	US-09-071-035-194	
45	7	1.8				

ALIGNMENTS

RESULT 1
US-08-435-149-2
; Sequence 2, Application US/08435149
; Patent No. 5866402
GENERAL INFORMATION:
; APPLICANT: INNIS, MICHAEL A.
; APPLICANT: ZAROR, ISABEL
; APPLICANT: CREASEY, ABIA A.
; TITLE OF INVENTION: CHIMERIC MCP AND DAF PROTEINS WITH CELL
; TITLE OF INVENTION: SURFACE LOCALIZING DOMAIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: EMERYVILLE
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,149
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0989,001
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 323 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-435-149-2
Query Match 84.8%; Score 323; DB 2; Length 323;
Best Local Similarity 100.0%; Pred No. 1.8e-306;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 DCGLPDPVNAQPALEGRTSFEDVITYIKCEESFYKIGEKDSYICLKGSQMSDIEFC 60
Qy 95 NNSCEVPTRLNASLKPITYTONYFVGTVEYECRPGYRRPRLSPKLTCLQNLKMS7A 154
Db 61 NNSCEVPTRLNASLKPITYTONYFVGTVEYECRPGYRRPRLSPKLTCLQNLKMS7A 120
Qy 155 VEFCKKSCPNNGEIRNGOIVPGGILFGATISFSCNTGYKLFGSTSSFCILSGSSVOMS 214
Db 121 VEFCKKSCPNNGEIRNGOIVPGGILFGATISFSCNTGYKLFGSTSSFCILSGSSVOMS 180
Qy 215 DPLPCEREIYCAPPOINDGIIQGERDHYGYROSATYACNKGFTMIGESITCTVNNDEG 274
Db 181 DPLPCEREIYCAPPOINDGIIQGERDHYGYROSATYACNKGFTMIGESITCTVNNDEG 240
Qy 275 EMSGPPPECRGKSLTSKVPPTVQKPTTVVPTTEVSPTSQKTTTTPPNAQATSTPVS 334
Db 241 EMSGPPPECRGKSLTSKVPPTVQKPTTVVPTTEVSPTSQKTTTTPPNAQATSTPVS 300
Qy 335 RTTKHFHETTPNKGSGTTSCTTR 357
Db 301 RTTKHFHETTPNKGSGTTSCTTR 323

RESULT 2

US-08-435-149-3
; Sequence 3, Application US/08435149
; Patent No. 5866402
; GENERAL INFORMATION:
; APPLICANT: INNIS, MICHAEL A.
; APPLICANT: ZAROR, ISABEL
; TITLE OF INVENTION: CHIMERIC MCP AND DAF PROTEINS WITH CELL
; TITLE OF INVENTION: SURFACE LOCALIZING DOMAIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: EMERYVILLE
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,149
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0989,001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; TELEEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 577 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-435-149-3

Query Match 84.8%; Score 323; DB 2; Length 577;
Best Local Similarity 100.0%; Pred. No. 3,1e-306;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 DCGLPDPVNAQPALEGRTSFEDVITYIKCEESFYKIGEKDSYICLKGSQMSDIEFC 94
|||||

Db 255 DCGLPDPVNAQPALEGRTSFEDVITYIKCEESFYKIGEKDSYICLKGSQMSDIEFC 314
Qy 95 NNSCEVPTRLNASLKPITYTONYFVGTVEYECRPGYRRPRLSPKLTCLQNLKMS7A 154
Db 315 NNSCEVPTRLNASLKPITYTONYFVGTVEYECRPGYRRPRLSPKLTCLQNLKMS7A 374
Qy 155 VEFCKKSCPNNGEIRNGOIVPGGILFGATISFSCNTGYKLFGSTSSFCILSGSSVOMS 214
Db 375 VEFCKKSCPNNGEIRNGOIVPGGILFGATISFSCNTGYKLFGSTSSFCILSGSSVOMS 434
Qy 215 DPLPCEREIYCAPPOINDGIIQGERDHYGYROSATYACNKGFTMIGESITCTVNNDEG 274
Db 435 DPLPCEREIYCAPPOINDGIIQGERDHYGYROSATYACNKGFTMIGESITCTVNNDEG 494
Qy 275 EMSGPPPECRGKSLTSKVPPTVQKPTTVVPTTEVSPTSQKTTTTPPNAQATSTPVS 334
Db 495 EMSGPPPECRGKSLTSKVPPTVQKPTTVVPTTEVSPTSQKTTTTPPNAQATSTPVS 554
Qy 335 RTTKHFHETTPNKGSGTTSCTTR 357
Db 555 RTTKHFHETTPNKGSGTTSCTTR 577

RESULT 3

US-09-475-460A-32
; Sequence 32, Application US/09475460A
; Patent No. 6316253
; GENERAL INFORMATION:
; APPLICANT: Scott, Elizabeth
; APPLICANT: Innis, Michael
; TITLE OF INVENTION: EXPRESSION VECTORS, TRANSFECTION SYSTEMS, AND METHOD OF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 1527,003
; CURRENT APPLICATION NUMBER: US/09/475,460A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 32
; LENGTH: 611
; TYPE: PRT
; ORGANISM: CAB2
US-09-475-460A-32

Query Match 84.8%; Score 323; DB 4; Length 611;
Best Local Similarity 100.0%; Pred. No. 3,2e-306;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 DCGLPDPVNAQPALEGRTSFEDVITYIKCEESFYKIGEKDSYICLKGSQMSDIEFC 94
Db 289 DCGLPDPVNAQPALEGRTSFEDVITYIKCEESFYKIGEKDSYICLKGSQMSDIEFC 348
Qy 95 NNSCEVPTRLNASLKPITYTONYFVGTVEYECRPGYRRPRLSPKLTCLQNLKMS7A 154
Db 349 NNSCEVPTRLNASLKPITYTONYFVGTVEYECRPGYRRPRLSPKLTCLQNLKMS7A 408
Qy 155 VEFCKKSCPNNGEIRNGOIVPGGILFGATISFSCNTGYKLFGSTSSFCILSGSSVOMS 214
Db 409 VEFCKKSCPNNGEIRNGOIVPGGILFGATISFSCNTGYKLFGSTSSFCILSGSSVOMS 468
Qy 215 DPLPCEREIYCAPPOINDGIIQGERDHYGYROSATYACNKGFTMIGESITCTVNNDEG 274
Db 469 DPLPCEREIYCAPPOINDGIIQGERDHYGYROSATYACNKGFTMIGESITCTVNNDEG 528
Qy 275 EMSGPPPECRGKSLTSKVPPTVQKPTTVVPTTEVSPTSQKTTTTPPNAQATSTPVS 334
Db 529 EMSGPPPECRGKSLTSKVPPTVQKPTTVVPTTEVSPTSQKTTTTPPNAQATSTPVS 588
Qy 335 RTTKHFHETTPNKGSGTTSCTTR 357
Db 589 RTTKHFHETTPNKGSGTTSCTTR 611

RESULT 4

US-09-748-061A-32
; Sequence 32, Application US/09748061A
; Patent No. 6451539
; GENERAL INFORMATION:
; APPLICANT: Scott, Elizabeth
; APPLICANT: Innis, Michael
; TITLE OF INVENTION: EXPRESSION VECTORS, TRANSFECTION SYSTEMS, AND METHOD OF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: P01527.101 / 2302-1527.10
; CURRENT APPLICATION NUMBER: US/09/748,061A
; CURRENT FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 32
; LENGTH: 611
; TYPE: PR1
; ORGANISM: CAB2
US-09-748-061A-32

Query Match 84.8%; Score 323; DB 4; Length 611;
Best Local Similarity 100.0%; Pred. No. 3.2e-306;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 DCGLPVPYNAQPALEGRTPEDVTITTKCESEFVKIPGEKDSVYICKGSQMSDIEEFC 94
DB 289 DCGLPVPYNAQPALEGRTPEDVTITTKCESEFVKIPGEKDSVYICKGSQMSDIEEFC 348
QY 95 NRSECEVPLNSASLAKOPYTONPEYGTVEYECRPGYRREPSLSPLTCTLOMLKMTA 154
DB 349 NRSECEVPLNSASLAKOPYTONPEYGTVEYECRPGYRREPSLSPLTCTLOMLKMTA 408
QY 155 VEFCKKSCPNPEIRNGQIDVPGLFGATISFCNTGYKLFGSTSFCLISSSVQWS 214
DB 409 VEFCKKSCPNPEIRNGQIDVPGLFGATISFCNTGYKLFGSTSFCLISSSVQWS 468
QY 215 DPLECRETICPAPPOIDNGIIGERDHYGYRQSVTYACNKGFTMIGHSIYCYVNNDEG 274
DB 469 DPLECRETICPAPPOIDNGIIGERDHYGYRQSVTYACNKGFTMIGHSIYCYVNNDEG 528
QY 275 EMGAPPEPCRGKSLTSKVPYVOKPTVNVPTTEVSPTSOCTTKTTPNMOATRSPTVS 334
DB 529 EMGAPPEPCRGKSLTSKVPYVOKPTVNVPTTEVSPTSOCTTKTTPNMOATRSPTVS 588
QY 335 RTTKHFHTTPNKGSGTTSCTTR 357
DB 589 RTTKHFHTTPNKGSGTTSCTTR 611

RESULT 5
US-08-310-416A-14
; Sequence 14, Application US/08310416A
; Patent No. 5679546
; GENERAL INFORMATION:
; APPLICANT: Jone-Long Ko et al.
; TITLE OF INVENTION: CHIMERIC PROTEINS WHICH BLOCK
; TITLE OF INVENTION: COMPLEMENT ACTIVATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,416A
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06180/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELE: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-310-416A-14

Query Match 71.7%; Score 273; DB 1; Length 324;
Best Local Similarity 100.0%; Pred. No. 8.7e-258;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 QMSDIEEFCNNSCEVPTPLNSASLAKOPYTONPVYGVYVEYECRPGYRREPSLSPLKLTG 145
DB 52 QMSDIEEFCNNSCEVPTPLNSASLAKOPYTONPVYGVYVEYECRPGYRREPSLSPLKLTG 111
QY 146 LONLKMSTAVFECKKSCPNPEIRNGQIDVPGLFGATISFCNTGYKLFGSTSFCL 205
DB 112 LONLKMSTAVFECKKSCPNPEIRNGQIDVPGLFGATISFCNTGYKLFGSTSFCL 171
QY 206 ISSGVQMSDPLPECRETICPAPPOIDNGIIGERDHYGYRQSVTYACNKGFTMIGHSI 265
DB 172 ISSGVQMSDPLPECRETICPAPPOIDNGIIGERDHYGYRQSVTYACNKGFTMIGHSI 231
QY 266 YCTVNNDEGMSGPPPECRGKSLTSKVPYVOKPTVNVPTTEVSPTSOCTTKTTPNA 325
DB 232 YCTVNNDEGMSGPPPECRGKSLTSKVPYVOKPTVNVPTTEVSPTSOCTTKTTPNA 291
QY 326 QATRSPTVSRRTTKHFHTTPNKGSGTTSCTRL 358
DB 292 QATRSPTVSRRTTKHFHTTPNKGSGTTSCTRL 324

RESULT 6
US-08-888-171-14
; Sequence 14, Application US/08888171
; Patent No. 5851528
; GENERAL INFORMATION:
; APPLICANT: Jone-Long, Ko
; APPLICANT: Higgins, Paul J.
; APPLICANT: Yeh, C. Grace
; TITLE OF INVENTION: METHODS OF INHIBITING COMPLEMENT
; TITLE OF INVENTION: ACTIVATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,171
; FILING DATE: 03-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,416
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.

PAGES: 1250-1250
DATE: 1991
US-09-133-944-16

Query Match 9.7%; Score 37; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 7.2e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTTSCTTRLISGHTCTTGLGTLVTMGLT 381
DB 1 PNKSGTTSCTTRLISGHTCTTGLGTLVTMGLT 37

RESULT 10
US-09-208-827-17
Sequence 17, Application US/09208827
Patent No. 6391582
GENERAL INFORMATION:
APPLICANT: Luo, Ying
APPLICANT: Yu, Pei Wen
APPLICANT: Lorens, James
TITLE OF INVENTION: SHUTTLE VECTORS
FILE REFERENCE: A66252-1/DB/DAV
CURRENT APPLICATION NUMBER: US/09/208,827
CURRENT FILING DATE: 1998-12-09
EARLIER APPLICATION NUMBER: 09/133,949
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 37
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: anchor site
PUBLICATION INFORMATION:
JOURNAL: Nature
VOLUME: 333
ISSUE: 6170
PAGES: 269-272
DATE: 1988
PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 266
PAGES: 1250-1250
DATE: 1991
US-09-208-827-17

Query Match 9.7%; Score 37; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 7.2e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTTSCTTRLISGHTCTTGLGTLVTMGLT 381
DB 1 PNKSGTTSCTTRLISGHTCTTGLGTLVTMGLT 37

RESULT 11
US-08-787-738B-16
Sequence 16, Application US/08787738B
Patent No. 6455247
GENERAL INFORMATION:
APPLICANT: Rothenburg, Michael S.
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
FILE REFERENCE: A-64259-1 correction
CURRENT APPLICATION NUMBER: US/08/787,738B
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 08/589,108
PRIOR FILING DATE: 1996-01-23
PRIOR APPLICATION NUMBER: 08/589,911
PRIOR FILING DATE: 1996-01-23

NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 37
TYPE: PRT
ORGANISM: Rattus sp.
US-08-787-738B-16

Query Match 9.7%; Score 37; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 7.2e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTTSCTTRLISGHTCTTGLGTLVTMGLT 381
DB 1 PNKSGTTSCTTRLISGHTCTTGLGTLVTMGLT 37

RESULT 12
US-09-157-748-19
Sequence 19, Application US/09157748
Patent No. 6461813
GENERAL INFORMATION:
APPLICANT: Lorens, James
TITLE OF INVENTION: Multiparameter FACS Assays to Detect Alterations in
FILE REFERENCE: A6587/DB/RMS
CURRENT APPLICATION NUMBER: US/09/157,748
CURRENT FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 37
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
JOURNAL: Nature
VOLUME: 333
ISSUE: 6170
PAGES: 269-272
DATE: 1988
PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 266
PAGES: 1250-
DATE: 1991
US-09-157-748-19

Query Match 9.7%; Score 37; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 7.2e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTTSCTTRLISGHTCTTGLGTLVTMGLT 381
DB 1 PNKSGTTSCTTRLISGHTCTTGLGTLVTMGLT 37

RESULT 13
US-08-004-492-4
Sequence 4, Application US/08004492
Patent No. 5623053
GENERAL INFORMATION:
APPLICANT: Gastinel, Louis N.
APPLICANT: Bjorkman, Pamela J.
TITLE OF INVENTION: Soluble Mammal-Derived FC Receptor Which Binds at a pH Rang
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shirley L. Church
STREET: 1063 Morse Avenue, #11-306
CITY: Sunnyvale
STATE: CA
COUNTRY: U.S.A.
ZIP: 94089
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: EPO Patentin 1.30/Edited in Microsoft Word 7.0, saved in "text onl
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/004,492
FILING DATE: 14-JAN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/819,413
FILING DATE: 10-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Church, Shirley L.
REGISTRATION NUMBER: 31,858
REFERENCE/DOCKET NUMBER: CIT2120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 745-1567
TELEFAX: (408) 747-1109
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acid residues
TYPE: Amino acid
STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: Protein/Peptide
HYPOTHETICAL: NO
ANTI-SENSE:
FRAGMENT TYPE: C-terminal fragment
ORIGINAL SOURCE:
ORGANISM: FcRn from Rattus norvegicus DAF from Homo sapiens
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: FcRn from 11 day old/germ-line
HAPLOTYPE:
TISSUE TYPE: FcRn from proximal third of small intestine
CELL TYPE: FcRn from epithelial cells
CELL LINE: DAF from Hela cells
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE: 'p-51-DAF' cell line produces chimeric FcRn heavy chain with
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: The insertion of the DAF amino acid sequence after the Fc
LOCATION: FcRn heavy chain (a.a. 265 to 269) from 1 to 5, DAF (a.a.
IDENTIFICATION METHOD: The cell surface expression of lipid-linked
OTHER INFORMATION: Intracellular modification results in the removal
PUBLICATION INFORMATION:
AUTHORS: Gastinel, Louis N.
AUTHORS: Simister, N.E.
AUTHORS: Bjorkman, P.J.
TITLE: Expression and Crystallization of a Soluble and Functional
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 89
ISSUE:
PAGES: 638-642
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 4: FROM 1 TO 42
US-08-004-492-4

Query Match 9.7%; Score 37; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.1e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 345 PKNKSGTSGTTRLISGHTCFITLGLGLTYMGLLT 381
|||||

DB 6 PKNKSGTSGTTRLISGHTCFITLGLGLTYMGLLT 42

RESULT 14
US-08-004-492-7
Sequence 7, Application US/08004492
Patent No. 5623053
GENERAL INFORMATION:
APPLICANT: Gastinel, Louis N.
APPLICANT: Bjorkman, Pamela J.
TITLE OF INVENTION: Soluble Mammal-Derived Fc Receptor Which Binds at a pH Rang
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Shirley L. Church
STREET: 1063 Morse Avenue, #11-306
CITY: Sunnyvale
STATE: CA
COUNTRY: U.S.A.
ZIP: 94089
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: EPO Patentin 1.30/Edited in Microsoft Word 7.0, saved in "text onl
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/004,492
FILING DATE: 14-JAN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/819,413
FILING DATE: 10-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Church, Shirley L.
REGISTRATION NUMBER: 31,858
REFERENCE/DOCKET NUMBER: CIT2120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 745-1567
TELEFAX: (408) 747-1109
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acid residues
TYPE: Amino acid
STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: Protein/Peptide
HYPOTHETICAL: NO
ANTI-SENSE:
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Beta 2-M from Rattus norvegicus DAF from Homo sapiens
STRAIN: Beta 2-M from Sprague-Dawley
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE: DAF from Hela cells
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Beta 2m-DAF' cell line produces chimeric rat beta 2-microglo
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: The insertion of the DAF amino acid sequence after the C-
LOCATION: Rat beta 2-microglobulin (a.a. 95 to 99) from 1 to 5 DAF
IDENTIFICATION METHOD: The cell surface expression of lipid-linked
OTHER INFORMATION: Intracellular modification results in the removal
PUBLICATION INFORMATION:
AUTHORS: Gastinel, Louis N.
AUTHORS: Simister, N.E.


```

:
:   AUTHORS: Bjorkman, P.J.
:   TITLE: Expression and Crystallization of a Soluble and Functional f
:   JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
:   VOLUME: 89
:   ISSUE:
:   PAGES: 638-642
:   DATE:
:   DOCUMENT NUMBER:
:   FILING DATE:
:   PUBLICATION DATE: 16-Jan-1992
:   RELEVANT RESIDUES IN SEQ ID NO: 7 : FROM 1 TO 42
:
US-08-004-492-7

Query Match          9.7%; Score 37; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.1e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTSGTTRLISGHTCTFLTGTLGTLVMTGLLT 381
Db 6 PNKSGTSGTTRLISGHTCTFLTGTLGTLVMTGLLT 42

RESULT 15
US-08-282-951-2
: Sequence 2, Application US/08282951
: Patent No. 5665590
: GENERAL INFORMATION:
: APPLICANT: YANG, ZHI
: TITLE OF INVENTION: METHOD FOR ISOLATING AND DIRECTLY
: TITLE OF INVENTION: CLONING GENES WHICH ENCODE CELL-SURFACE AND SECRETED
: TITLE OF INVENTION: PROTEINS
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Morrlson & Foerster
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/282,951
: FILING DATE: 29-JUL-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: LEHNHARDT, SUSAN K.
: REGISTRATION NUMBER: 33,943
: REFERENCE/DOCKET NUMBER: 20296-20012.00
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 706141
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 102 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-08-282-951-2

Query Match          9.7%; Score 37; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.8e-28;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 PNKSGTSGTTRLISGHTCTFLTGTLGTLVMTGLLT 381
Db 65 PNKSGTSGTTRLISGHTCTFLTGTLGTLVMTGLLT 101
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Search completed: February 12, 2003, 11:12:18
Job time : 17 secs

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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:09:06 ; Search time 35 Seconds
(without alignments)
2242.970 Million cell updates/sec

Title: US-09-623-035-2
Perfect score: 381
Sequence: 1 MTVARPSVPALPLAGELPR.....HTCFTLGLGLTWTMGLTR 381

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp-phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_unclassified:*
- 14: sp_virus:*
- 15: sp_bacteriophage:*
- 16: sp_bacteriophage:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	225	59.1	265 4	Q8TD12
2	197	51.7	419 4	Q8TD11
3	197	51.7	422 4	Q8TD13
4	148	38.8	347 6	Q9MYJ6
5	117	30.7	316 4	Q8TD14
6	99	26.0	305 6	Q9MYJ5
7	99	26.0	347 6	Q9MYJ7
8	35	14.4	55 6	Q18722
9	28	7.3	51 6	Q18724
10	24	6.3	343 6	Q9MYJ4
11	24	6.3	343 6	Q9MYJ3
12	22	5.8	271 6	Q9MYJ0
13	22	5.8	278 6	Q9MYJ1
14	22	5.8	343 6	Q9MYJ2
15	22	5.8	343 6	Q9MYJ9
16	22	5.8	343 6	Q9MYJ9

17	15	3.9	63	6	Q18726	018726 ateles geof
18	14	3.7	51	6	Q18723	018723 macaca fusc
19	13	3.4	51	6	Q18727	018727 cebus apell
20	10	2.6	326	6	Q9GLM1	Q9GLM1 sus scrofa
21	10	2.6	341	6	Q9GLM2	Q9GLM2 sus scrofa
22	10	2.6	390	11	Q921P0	Q921P0 mus musculus
23	10	2.6	498	6	Q9GLM0	Q9GLM0 sus scrofa
24	10	2.6	550	12	P88903	P88903 kaposi's sa
25	10	2.6	550	12	Q40912	Q40912 kaposi's sa
26	9	2.4	345	6	Q95LH0	Q95LH0 pan troglod
27	9	2.4	2470	13	Q90681	Q90681 gallus gall
28	8	2.1	185	2	Q9ALJ2	Q9ALJ2 chlorobium
29	8	2.1	202	10	Q9FE27	Q9FE27 arabidopsis
30	8	2.1	204	10	Q9CAX3	Q9CAX3 arabidopsis
31	8	2.1	217	2	Q93AG4	Q93AG4 azotobacter
32	8	2.1	227	2	Q9AKU1	Q9AKU1 prosthecoc
33	8	2.1	290	2	Q8VNU7	Q8VNU7 chlorobium
34	8	2.1	292	2	Q8VNU0	Q8VNU0 chlorobium
35	8	2.1	292	2	Q8VMT4	Q8VMT4 prosthecoc
36	8	2.1	324	5	Q44840	Q44840 caenorhabd
37	8	2.1	363	6	Q02839	Q02839 sus scrofa
38	8	2.1	413	16	Q9RZM5	Q9RZM5 delinococcus
39	8	2.1	426	16	Q8Z2E6	Q8Z2E6 yersinia pe
40	8	2.1	502	11	Q9ER55	Q9ER55 mus musculu
41	8	2.1	533	11	Q08569	Q08569 cavia porce
42	8	2.1	578	3	Q96V96	Q96V96 orpiniomyces
43	8	2.1	732	10	Q94HA5	Q94HA5 oryza sativ
44	8	2.1	2967	12	Q41892	Q41892 hepatitis g
45	8	2.1	11721	4	Q8WX17	Q8WX17 homo sapien

ALIGNMENTS

RESULT 1

ID Q8TD12 PRELIMINARY; PRT; 265 AA.
AC Q8TD12;
-DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Decay-accelerating factor 3 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hindmarsh E.J., Marks R.M.;
RT "Molecular analysis of human decay-accelerating factor: eight novel
isoforms generated by intron retention and alternative splicing."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057579; AAL25834.1; -.
FT NON_TER
SQ SEQUENCE 265 AA; 29370 MW; 3FED6E3F84A79421 CRC64;

Query Match	59.1%	Score 225	DB 4	Length 265
Best local similarity	100.0%	Pred. No. 7e-219		
Matches 225; Conservative	0;	Mismatches	0;	Indels
			0;	Gaps
				0;
QY 130 RGYRREPSLSPKLTCLNLKSTAVEFCCKKSCPNPGRIRNGOIDVPGILFGATISFS 189				
DB 1 RGYRREPSLSPKLTCLNLKSTAVEFCCKKSCPNPGRIRNGOIDVPGILFGATISFS 60				
QY 190 CNTGYKLFSGTSSFCLLIGSSVQWSDPLPECREIYCPAPQIDNGIIGERDHYGROSV 249				
DB 61 CNTGYKLFSGTSSFCLLIGSSVQWSDPLPECREIYCPAPQIDNGIIGERDHYGROSV 120				
QY 250 TYACKGFTMIGEHISYICVNNDEGEMSGPPRECKGKSLTSVPTVYKPTTVNPTTEV 309				
DB 121 TYACKGFTMIGEHISYICVNNDEGEMSGPPRECKGKSLTSVPTVYKPTTVNPTTEV 180				
QY 310 SPTSGKTTTNTTTPNAQATRSPTVSRTRTKHFHETTPNKGSGTTS 354				

Db 181 SPTSOKTTTCTTTPNAQTRSTPVSRTTKHHEHTPNKSGSTISG 225

RESULT 2

Q8TD11 PRELIMINARY; PRT; 419 AA.

AC 08TD11: 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hindmarsh E.J., Marks R.M.;
RT "Molecular analysis of human decay-accelerating factor: eight novel
isoforms generated by intron retention and alternative splicing."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY055760; AAL25835.1; -
FT NON_TER 1
SQ SEQUENCE 419 AA; 44796 MW; FACE7E75072A7ESC CRC64;

Query Match 51.7%; Score 197; DB 4; Length 419;
Best Local Similarity 100.0%; Pred. No. 2.1e-190;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 RPYRRRPSLSPKLTCLONLKWSTAVFERCKKSCPNPGEIRNGQIDVPGILFGATISFS 189
Db 1 RPYRRRPSLSPKLTCLONLKWSTAVFERCKKSCPNPGEIRNGQIDVPGILFGATISFS 60
Qy 190 CMTGYKLFGSTSFCLISGSSVQMSDPLPECRELYCPAPQIDNGIIGERDHYGYSQSV 249
Db 61 CMTGYKLFGSTSFCLISGSSVQMSDPLPECRELYCPAPQIDNGIIGERDHYGYSQSV 120
Qy 250 TYACNKGFTMIGHSIYCTVNNDEGEMSGPPPECRGKSLTSKVPYVOKPTTVVPTTEV 309
Db 121 TYACNKGFTMIGHSIYCTVNNDEGEMSGPPPECRGKSLTSKVPYVOKPTTVVPTTEV 180
Qy 310 SPTSOKTTTCTTTPNAQ 326
Db 181 SPTSOKTTTCTTTPNAQ 197

RESULT 3
Q8TD13 PRELIMINARY; PRT; 422 AA.

AC 08TD13: 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hindmarsh E.J., Marks R.M.;
RT "Molecular analysis of human decay-accelerating factor: eight novel
isoforms generated by intron retention and alternative splicing."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY055758; AAL25833.1; -
FT NON_TER 1
SQ SEQUENCE 422 AA; 44849 MW; 7BD89A886CCCD18E CRC64;

Query Match 51.7%; Score 197; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 2.1e-190;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 RPYRRRPSLSPKLTCLONLKWSTAVFERCKKSCPNPGEIRNGQIDVPGILFGATISFS 189
Db 1 RPYRRRPSLSPKLTCLONLKWSTAVFERCKKSCPNPGEIRNGQIDVPGILFGATISFS 60
Qy 190 CMTGYKLFGSTSFCLISGSSVQMSDPLPECRELYCPAPQIDNGIIGERDHYGYSQSV 249
Db 61 CMTGYKLFGSTSFCLISGSSVQMSDPLPECRELYCPAPQIDNGIIGERDHYGYSQSV 120
Qy 250 TYACNKGFTMIGHSIYCTVNNDEGEMSGPPPECRGKSLTSKVPYVOKPTTVVPTTEV 309
Db 121 TYACNKGFTMIGHSIYCTVNNDEGEMSGPPPECRGKSLTSKVPYVOKPTTVVPTTEV 180
Qy 310 SPTSOKTTTCTTTPNAQ 326
Db 181 SPTSOKTTTCTTTPNAQ 197

RESULT 4

Q9MYJ6 PRELIMINARY; PRT; 347 AA.

AC 09MYJ6: 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20368351; PubMed=10906393;
RA Kuttner-Kondoa L., Baia Subramanian V., Atkinson J.P., Yua J.,
Medofa M.E.;
RT "Conservation in decay accelerating factor (DAF) structure among
primates."
RL Dev. Comp. Immunol. 24:815-827(2000).
DR EMBL: AF149760; AAF73176.1; -
DR HSSP: P08603; IHCC.
DR InterPro: IPR000436; Sush1_SCR_CCP.
DR Pfam: PF00084; sush1_4.
DR SMART: SM00032; CCP; 4.
FT NON_TER 1
SQ SEQUENCE 347 AA; 37872 MW; B03CDAE5DA51BA2 CRC64;

Query Match 38.8%; Score 148; DB 6; Length 347;
Best Local Similarity 100.0%; Pred. No. 6.1e-141;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 225 CPAPQIDNGIIGERDHYGYSQSVTYACNKGFTMIGHSIYCTVNNDEGEMSGPPPECR 284
Db 191 CPAPQIDNGIIGERDHYGYSQSVTYACNKGFTMIGHSIYCTVNNDEGEMSGPPPECR 250
Qy 285 GKSLTSKVPYVOKPTTVVPTTEVSPTSOKTTTCTTTPNAQTRSTPVSRTTKHHEHT 344
Db 251 GKSLTSKVPYVOKPTTVVPTTEVSPTSOKTTTCTTTPNAQTRSTPVSRTTKHHEHT 310
Qy 345 PNKSGSTTTRLLSGHTFTLGLG 372
Db 311 PNKSGSTTTRLLSGHTFTLGLG 338

RESULT 5

Q8TD14 PRELIMINARY; PRT; 316 AA.

AC 08TD14: 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hindmarsh E.J.; Marks R.M.;
RT "Molecular analysis of human decay-accelerating factor: eight novel
isoforms generated by intron retention and alternative splicing."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055757; AAL25832.1; -
FT NON_TER 1
SQ SEQUENCE 316 AA; 33419 MW; DDE6BE56368C6778 CRC64;

Query Match 30.7%; Score 117; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.2e-109;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 210 SVQMSDPLPECRETYCAPPOIDNGIIGERDHYGRQSVTYACNKGKGTMTGHSITCTV 269
DB 1 SVQMSDPLPECRETYCAPPOIDNGIIGERDHYGRQSVTYACNKGKGTMTGHSITCTV 60
OY 270 NNDGEMSGPPECKGKSLTSKVPPTVQKPTTVNVPTEVSPTSOKTTKTTTNAQ 326
DB 61 NNDGEMSGPPECKGKSLTSKVPPTVQKPTTVNVPTEVSPTSOKTTKTTTNAQ 117

RESULT 6
O9MYJ5 PRELIMINARY; PRT; 305 AA.
AC O9MYJ5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Decay-accelerating factor (Fragment).
GN CD55
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20368351; PubMed=10906393;
RA Kuttner-Konda L., Bala Subramanian V., Atkinson J.P., Yua J.,
RA Medofa M.E.;
RT "Conservation in decay accelerating factor (DAF) structure among
primates."
RL Dev. Comp. Immunol. 24:815-827(2000).
DR EMBL; AF149761; AAF73177.1; -
DR HSP; P08603; IHCI.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00084; sush1; 4.
DR SMART; SM00032; CCP; 4.
FT NON_TER 1
SQ SEQUENCE 305 AA; 33508 MW; F72A8F398A7C353A CRC64;

Query Match 26.0%; Score 99; DB 6; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.9e-91;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 VPNAOPALEGRTSPEDVTYKCEESFYKIPGKDYICLKGSQMSIEFNCNSCVP 101
DB 8 VPNAOPALEGRTSPEDVTYKCEESFYKIPGKDYICLKGSQMSIEFNCNSCVP 67
OY 102 TRLSASLKOPIYTONFPVGTVEYECRPGYRRPSPS 140
DB 68 TRLSASLKOPIYTONFPVGTVEYECRPGYRRPSPS 106

RESULT 7
O9MYJ7 PRELIMINARY; PRT; 347 AA.
AC O9MYJ7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Decay-accelerating factor (Fragment).
GN CD55.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20368351; PubMed=10906393;
RA Kuttner-Konda L., Bala Subramanian V., Atkinson J.P., Yua J.,
RA Medofa M.E.;
RT "Conservation in decay accelerating factor (DAF) structure among
primates."
RL Dev. Comp. Immunol. 24:815-827(2000).
DR EMBL; AF149759; AAF73175.1; -
DR HSP; P08603; IHFI.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00084; sush1; 4.
DR SMART; SM00032; CCP; 4.
FT NON_TER 1
SQ SEQUENCE 347 AA; 37873 MW; 6DD4AB6C92F89D0 CRC64;

Query Match 26.0%; Score 99; DB 6; Length 347;
Best Local Similarity 100.0%; Pred. No. 2.1e-91;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 250 TYACNKGKGTMTGHSITCTVNNDEGEMSGPPECKGKSLTSKVPPTVQKPTTVNVPTEV 309
DB 216 TYACNKGKGTMTGHSITCTVNNDEGEMSGPPECKGKSLTSKVPPTVQKPTTVNVPTEV 275
OY 310 SPTSOKTTKTTTNAQATRSTPVSRTHKHETTPNG 348
DB 276 SPTSOKTTKTTTNAQATRSTPVSRTHKHETTPNG 314

RESULT 8
O18722 PRELIMINARY; PRT; 55 AA.
AC O18722;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Complement decay-accelerating factor (CD55) (Fragment).
GN DAF.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=98099759; PubMed=9435343;
RA Nonaka M., Nonaka M., Takenaka O., Okada N., Okada H.;
RT "A new repetitive sequence uniquely present in the decay-accelerating
factor genes."
RL Immunogenetics 47:246-255(1998).
CC -1- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY
STIMULITY).
CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
(RCA) FAMILY.
DR EMBL; AB003313; BAA22901.1; -
KW Complement pathway.
FT NON_TER 1
SQ SEQUENCE 55 AA; 5946 MW; 54FDF4CEE32C1ED9 CRC64;

Query Match 14.4%; Score 55; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.3e-47;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 291 KVPPTVQKPTTVNVPTEVSPTSOKTTKTTTNAQATRSTPVSRTHKHETTP 345

Db 1 KVPPTVOKPTTVNPTTEVSPTSOKTTTNTTTPNAOATRSTPVSRITKHFHTTP 55

RESULT 9

ID 018724 PRELIMINARY; PRT; 51 AA.

AC 018724;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DE Complement decay-accelerating factor (CD55) (Fragment).

GN DAF.

OS Hylobates syndactylus (Siamaang).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.

OX NCBI_TaxID=9590;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BLOOD;

RX MEDLINE=98099759; PubMed=9435343;

RA Nonaka M., Nonaka M., Takenaka O., Okada N., Okada H.;

RT "A new repetitive sequence uniquely present in the decay-accelerating factor genes.";

RL Immunogenetics 47:246-255(1998).

CC -1- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION (RCA) FAMILY.

CC EMBL: AB003316; BAA22904.1; -.

DR Complement pathway.

KW NON_TER 1 51

FT 1

SO SEQUENCE 51 AA; 5514 MW; ED112B05D2A87DC6 CRC64;

QY 291 KVPPTVOKPTTVNPTTEVSPTSOKTTT 318

Db 1 KVPPTVOKPTTVNPTTEVSPTSOKTTT 28

RESULT 10

ID 018725 PRELIMINARY; PRT; 51 AA.

AC 018725;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE Complement decay-accelerating factor (CD55) (Fragment).

GN DAF.

OS Hylobates lar (Common gibbon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.

OX NCBI_TaxID=9580;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BLOOD;

RX MEDLINE=98099759; PubMed=9435343;

RA Nonaka M., Nonaka M., Takenaka O., Okada N., Okada H.;

RT "A new repetitive sequence uniquely present in the decay-accelerating factor genes.";

RL Immunogenetics 47:246-255(1998).

CC -1- FUNCTION: PROTECTION OF CELLS FROM COMPLEMENT-MEDIATED DAMAGE (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION (RCA) FAMILY.

CC EMBL: AB003317; BAA22905.1; -.

DR Complement pathway.

KW NON_TER 1 51

FT 1

SO SEQUENCE 51 AA; 5514 MW; ED112B05D2A87DC6 CRC64;

Query Match 7.3%; Score 28; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.5e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 291 KVPPTVOKPTTVNPTTEVSPTSOKTTT 318

Db 1 KVPPTVOKPTTVNPTTEVSPTSOKTTT 28

RESULT 11

ID 09MYJ4 PRELIMINARY; PRT; 343 AA.

AC 09MYJ4;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Decay-accelerating factor (Fragment).

GN CD55.

OS Papio hamadryas (Hamadryas baboon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecidae;

OC Cercopithecoidea; Papio.

OX NCBI_TaxID=9557;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20368351; PubMed=10906393;

RA Kuttner-Kondoa L., Bala Subramanian V., Atkinson J.P., Yua J., Medofa M.E.;

RT "Conservation in decay accelerating factor (DAF) structure among primates.";

RL Dev. Comp. Immunol. 24:815-827(2000).

DR HSSP: P08603; IHLI.

DR InterPro: IPR001969; Aspprotease.site.

DR InterPro: IPR000436; Sushi_SCR_CCP.

DR Pfam: PF00084; sushi; 4.

DR SMART: SM00032; CCP; 4.

DR PROSITE: PS00141; ASP_PROTEASE; UNKNOWN_1.

KW NON_TER 1 1

FT 1

SO SEQUENCE 343 AA; 37465 MW; 828D47652F68A0C CRC64;

QY 217 LPFCREIYCPAPPOINDGIIGER 240

Db 183 LPFCREIYCPAPPOINDGIIGER 206

RESULT 12

ID 09MYJ3 PRELIMINARY; PRT; 343 AA.

AC 09MYJ3;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE Decay-accelerating factor (Fragment).

GN CD55.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecidae;

OC Cercopithecoidea; Macaca.

OX NCBI_TaxID=9544;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20368351; PubMed=10906393;

RA Kuttner-Kondoa L., Bala Subramanian V., Atkinson J.P., Yua J., Medofa M.E.;

RT "Conservation in decay accelerating factor (DAF) structure among primates.";

RL Dev. Comp. Immunol. 24:815-827(2000).

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DR EMBL: AF149763; AAF73179.1; -.
DR HSSP: P08603; IHFI.
DR InterPro: IPR000436; Sush1_SCR_CCP.
DR Pfam: PF00084; sush1; 4.
DR SMART: SM00032; CCP; 4.
FT NON_TER 1
SQ SEQUENCE 343 AA; 37296 MW; 2F04847C77316797 CRC64;

Query Match
Best Local Similarity 100.0%; Score 24; DB 6; Length 343;
Pred. No. 1.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 LPECREICPAPQIDNGIIGER 240
DB 183 LPECREICPAPQIDNGIIGER 206
|||||

RESULT 13
Q9MYJ0 PRELIMINARY; PRT; 271 AA.
ID Q9MYJ0
AC Q9MYJ0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Decay-accelerating factor (Fragment).
GN CD55.
OS Erythrocebus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN#B289;
RX MEDLINE=20368351; PubMed=10906393;
RA Kuttner-Kondoa L., Bala Subramanian V., Atkinson J.P., Yua J.,
RA Medofa M.E.;
RT "Conservation in decay accelerating factor (DAF) structure among
RT primates.";
RL Dev. Comp. Immunol. 24:815-827(2000).
DR EMBL: AF149766; AAF73182.1; -.
DR HSSP: P08603; IHFI.
DR InterPro: IPR000436; Sush1_SCR_CCP.
DR Pfam: PF00084; sush1; 4.
DR SMART: SM00032; CCP; 4.
FT NON_TER 1
SQ SEQUENCE 271 AA; 29897 MW; 27C36E5CFC3D921 CRC64;

Query Match
Best Local Similarity 100.0%; Score 22; DB 6; Length 271;
Pred. No. 1.2e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 LPECREICPAPQIDNGIIG 238
DB 183 LPECREICPAPQIDNGIIG 204
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RESULT 14
Q9MYJ1 PRELIMINARY; PRT; 278 AA.
ID Q9MYJ1
AC Q9MYJ1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Decay-accelerating factor (Fragment).
GN CD55.
OS Erythrocebus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN#B289;
RX MEDLINE=20368351; PubMed=10906393;
RA Kuttner-Kondoa L., Bala Subramanian V., Atkinson J.P., Yua J.,
RA Medofa M.E.;
RT "Conservation in decay accelerating factor (DAF) structure among
RT primates.";
RL Dev. Comp. Immunol. 24:815-827(2000).
DR EMBL: AF149765; AAF73181.1; -.
DR HSSP: P08603; IHFI.
DR InterPro: IPR000436; Sush1_SCR_CCP.
DR Pfam: PF00084; sush1; 4.
DR SMART: SM00032; CCP; 4.
FT NON_TER 1
SQ SEQUENCE 278 AA; 30607 MW; BF9286DBF703D08F CRC64;

Query Match
Best Local Similarity 100.0%; Score 22; DB 6; Length 278;
Pred. No. 1.2e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 LPECREICPAPQIDNGIIG 238
DB 183 LPECREICPAPQIDNGIIG 204
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RESULT 15
Q9MYJ2 PRELIMINARY; PRT; 343 AA.
ID Q9MYJ2
AC Q9MYJ2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Decay-accelerating factor (Fragment).
GN CD55.
OS Erythrocebus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN#B289;
RX MEDLINE=20368351; PubMed=10906393;
RA Kuttner-Kondoa L., Bala Subramanian V., Atkinson J.P., Yua J.,
RA Medofa M.E.;
RT "Conservation in decay accelerating factor (DAF) structure among
RT primates.";
RL Dev. Comp. Immunol. 24:815-827(2000).
DR EMBL: AF149764; AAF73180.1; -.
DR HSSP: P08603; IHFI.
DR InterPro: IPR000436; Sush1_SCR_CCP.
DR Pfam: PF00084; sush1; 4.
DR SMART: SM00032; CCP; 4.
FT NON_TER 1
SQ SEQUENCE 343 AA; 37423 MW; 6D5DEBADB3DC2112 CRC64;

Query Match
Best Local Similarity 100.0%; Score 22; DB 6; Length 343;
Pred. No. 1.4e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 LPECREICPAPQIDNGIIG 238
DB 183 LPECREICPAPQIDNGIIG 204
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Search completed: February 12, 2003, 11:11:28
Job time : 37 secs
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